

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 09:17:11 ; Search time 4372 Seconds  
(without alignments)  
10163.182 Million cell updates/sec

Title: US-10-690-246A-1

Perfect score: 917  
1 accgagagatagtagagagag.....ttttgtttgtttttcgg 917

Scoring table: IDENTITY NUC  
Gapop 10'-0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmb1:\*  
1: gb\_da:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	910	99.2	910	AY378149	AY378149 Phalaenop
2	359.4	35.2	1030	AY378148	AY378148 Phalaenop
3	339.2	37.0	942	AY196350	AY196350 Oncidium
4	335	36.5	952	AB094964	AB094964 Asparagus
5	324.2	35.4	1028	AY378147	AY378147 Phalaenop
6	316.8	34.5	980	AY378150	AY378150 Phalaenop
7	304.2	33.2	1005	AB071138	AB071138 Lilium re
8	299.4	32.6	1039	AF503913	AF503913 Lilium lo
9	295.6	32.2	933	AF209729	AF209729 Hemerocal
10	292.8	31.9	938	AF230706	AF230706 Tacca cha
11	285.4	31.1	651	AY337750	AY337750 Eupomatia
12	283.4	31.1	651	AY337751	AY337751 Eupomatia
13	284.8	31.1	852	AB050649	AB050649 Magnolia
14	282.6	30.8	830	AY621154	AY621154 Alpinia h
15	282.2	30.8	1002	AB094965	AB094965 Tulipa ge
16	265.8	29.0	1016	AB094966	AB094966 Tulipa ge
17	264.4	28.8	830	AY397762	AY397762 Chloranth
18	263	28.7	1084	AB003323	AB003323 Oryza sat
19	263	28.7	1210	AK069317	AK069317 Oryza sat

20	261	28.5	896	8	AY627630	AY627630 Akebia tr
21	260	28.4	1061	8	AF077760	AF077760 Oryza sat
22	259	28.2	768	8	AY436722	AY436722 Drimys wi
23	256.2	27.9	851	8	AY436723	AY436723 Drimys wi
24	255.4	27.9	810	8	AY436725	AY436725 Drimys wi
25	254.4	27.7	1008	8	AF052874	AF052874 Papaver n
26	254.2	27.6	1166	8	AY541065	AY541065 Hordeum v
27	253	27.6	809	8	AY436724	AY436724 Drimys wi
28	253	27.6	828	8	ACAA19959	ACAA19959 Asarum ca
29	251	27.4	959	8	AB007508	AB007508 Triticum
30	247.4	27.0	834	8	ACAA19955	ACAA19955 Asarum ca
31	245.8	26.8	852	8	AY436715	AY436715 Saruma he
32	239.4	26.1	906	8	GHY9724	GHY9724 Gerbera h
33	239.4	26.1	958	8	AY627631	AY627631 Akebia tr
34	238.6	26.0	643	8	TAB577377	TAB577377 Triticum
35	238.6	26.0	1083	8	AB107993	AB107993 Triticum
36	238.4	26.0	935	8	AY436736	AY436736 Lindeba e
37	236	25.7	1257	6	CQ855034	CQ855034 Sequence
38	236	25.7	1257	6	AX478035	AX478035 Sequence
39	235	25.6	1004	8	AF230697	AF230697 Asarum eu
40	233.4	25.5	810	8	AY337748	AY337748 Persea am
41	231.4	25.2	603	8	AY337748	AY337748 Platanus
42	229.8	25.1	763	8	AY162881	AY162881 Sequence
43	228	24.9	946	6	AR372458	AR372458 Sequence
44	227.2	24.8	681	6	AR372459	AR372459 Sequence
45	226.8	24.7	755	8	AF230699	AF230699 Calycanth

#### ALIGNMENTS

RESULT 1  
AY378149  
LOCUS  
DEFINITION  
Phalaenopsis equestris MADS box transcription factor (MADS2) mRNA,  
complete cds.  
AY378149  
ACCESSION  
AY378149.1 GI:38680584  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Phalaenopsis equestris  
Phalaenopsis equestris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
Epiphytaceae; higher Epiphytaceae; Vandaceae; Aseridaceae;  
Phalaenopsis.  
1 (bases 1 to 910)  
Tsai,W.C., Kuo,H.C.S., Chuang,M.H., Chen,W.H. and Chen,H.H.  
Four DBF-like MADS Box Genes Displayed Distinct Floral  
Morphogenetic Roles in Phalaenopsis Orchid  
Plant Cell Physiol. 45 (7), 831-844 (2004)  
JOURNAL  
PUBMED  
15295066  
REFERENCE  
2 (bases 1 to 910)  
Tsai,W.C., Chen,W.H. and Chen,H.H.  
Direct Submission  
Submitted (02-SRP-2003) Department of Biology, National Cheng Kung  
University, 1 University Rd., Tainan, Taiwan 701, Republic of China  
Location/Qualifiers  
1. 910  
/organism="Phalaenopsis equestris"  
/mol\_type="mRNA"  
/db\_xref="taxon:78828"  
/tissue\_type="flower bud"  
1. 910  
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/note="PcMADS2"  
69. 752  
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LIMFSSTCKLADYCSPTDIDKIGIERVQVLTGMGLMNAQYRMQNTLKLHININLR



Db 542 GATTAAATCTTAATCTTCAGAGAGATMAACAGAGAGAGAGAGAGATCTCGAAGGCTT 601  
 Qy 423 GACATTAAGCAATCGCGCGCTTTGAGCAAACTTTGAAAGAGCTCTTGAATTTGTAG 482  
 Db 602 GGGCGTTAAAGAGCTGCGCGCTTTGAGCAAAATTTGAGAGAGCTCGTTAAGATTGTCG 661  
 Qy 483 GCATAGAAAGTATCATGTGATCGCCACACAAATCGACATTCACAAAAAGCTTAAAG 542  
 Db 662 GCAGAGAAAGTATCATGTGATCGTACGCAAAACAGACCTTCAGAAAAAGCTCAAAAG 721  
 Qy 543 CACAGAGAAACTTACCGCGCTCTTAATCATGAACTGATTA---TGAAGAGAGAAATCC 599  
 Db 722 CAGCAGACAATATATACAGAGCCCTTACGCAATGAACTGAGAGAGCTGAGAGAAATCA 781  
 Qy 600 GAATGAGGTTTAAATGTAAGAAACAGAGTAAATTTATGAAATTCGATTCGATGAT 659  
 Db 782 ACCGTGAGATTCTCTCGTAAGAGATCTTAAGCTGATCTATGACAGCTCAATCTCAATGCG 841  
 Qy 660 GAATGAGTGTCTCAGAG 676  
 Db 842 AATCGGCTGCACCGGA 858

RESULT 3  
 AY196350 942 bp mRNA linear PLN 02-MAR-2003  
 LOCUS Oncidium cv. 'Gower Ramsey' MADS box protein (MADS3) mRNA, complete  
 DEFINITION cds.  
 ACCESSION AY196350  
 VERSION AY196350.1 GI:28630894  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 .  
 Oncidium cv. 'Gower Ramsey',  
 Oncidium cv. 'Gower Ramsey',  
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 Epidendroideae; higher Epidendroideae; Maxillarieae; Oncidiinae;  
 Oncidium.  
 1 (bases 1 to 942)  
 Hsu, H.-F. and Yang, C.-H.  
 An Orchid (Oncidium Gower Ramsey) Ap3-like MADS Gene Regulates  
 Floral Formation and Initiation  
 Plant Cell Physiol. 43 (10), 1198-1209 (2002)  
 JOURNAL MEDLINE 22294943  
 PUBMED 12407200  
 REFERENCE 2 (bases 1 to 942)  
 Hsu, H.-F. and Yang, C.-H.  
 Direct Submission  
 Submitted (14-DEC-2002) Graduate Institute of Biotechnology,  
 National Chung-Hsing University, 250 Kuo-Kuang Rd., Taichung,  
 Taiwan 40227, Republic of China  
 JOURNAL  
 AUTHORS  
 TITLE  
 FEATURES  
 source  
 1. .942  
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 /cultivar="Gower Ramsey"  
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 /note="OMADS3"  
 121. .735  
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 /note="similar to AP3"  
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 MEIRORKEGLEDVYKELRGLEKLESIKIVRKRKHVIVATQDTYKKKLSTREM  
 YFALNLEQLEVDENQKRSFIADSLSDSGVNSAISANQRLAHCL"

ORIGIN

Query Match 37.0%; Score 339.2; DB 8; Length 942;  
 Best Local Similarity 74.0%; Pred. No. 16-67;  
 Matches 444; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

Qy 72 AGAGATGGGGAGGGAGAGATAGATTAATAAAGATAGAAATCCAGCAACAGGCAAGT 131  
 Db 117 AGCAATGGGAGAGGAAAGATAGATTAAGAAAGATAGAAATCCAAACAGGCAAGT 176  
 Qy 132 TACATATTTAAGAGAGAGATTGGATATCTGAAGAAAGCCAGAGAGCTCATCTTCTCG 191  
 Db 177 AACTTACTCAAAAGAGGAGCTTGAATTAACGAAAAAGCCATGAAATTAACAGTGTCTG 236  
 Qy 192 TGATGCTCAGGCTCTCTCATCATGTTCTCAAGCACAGAAAGTTGGCTGATTAAGTCTG 251  
 Db 237 CGAGGCTAAGGTTTCTCTCATCATGTTCTCAAGCTCTGGCAATTAATCTGATTAAGTCTG 296  
 Qy 252 CCCCTTACTGATTAATTAAGGGATATATGAGAGTACAGAGTTGTGATCTGAAATGATCT 311  
 Db 297 CCTTCTACAGAAATCAAAAGATGCGTTTCAGAGGTATCAGCAAGTTACCGGCTTGAAT 356  
 Qy 312 ATGGAATGCTCAGTATGAGAGATGCAATACCTGAGCATCTGAATGATTAACCA 371  
 Db 357 CTGGAGTCCCAATACAGAGAGATGCAAGTACTTGATGATCTCAGAGAGGTTATCA 416  
 Qy 372 AAACCTGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 431  
 Db 417 TAACTTCAATGAGATGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGATTAAGAT 476  
 Qy 432 GCACTGCGCGGCTTTGAGCAAACTTTGAAAGTCTTTAGAAATTTGAGGATAGAAA 491  
 Db 477 GGAATCGCGGCTTTGAGCAAAATTTGAAAGTCTTTAGAAATTTGAGGATAGAAA 536  
 Qy 492 GTATCATGTGATGCGCACACAACTGACCTTACAGAAAAAGCTTAAAGCACAAAGGA 551  
 Db 537 GTATCATGTGATGCGCACACAACTGACCTTACAGAAAAAGCTTAAAGCACAAAGGA 596  
 Qy 552 AACTTACCGGCTTTATATGATGACT---GGAATGAAAGAGAGAAATCGAATCAAG 608  
 Db 597 AATGTACCCAGCCCTTATGATGATGCTGACAGAGAGTGTGATGATGATCAACAGCGCAG 656  
 Qy 609 TTTTATGTGAAAAACAGAGTAAATTTATGAAATTTGAAATTTGAAATTTGAAATTTG 668  
 Db 657 TTTTATGTGAAAAATCTTAAGCGGTGTCTCAACAGGCAATCTCAATGGGAGATCAGAG 716

RESULT 4  
 AB094964 952 bp mRNA linear PLN 29-APR-2003  
 LOCUS Asparagus officinalis AODEF mRNA for MADS-box transcription factor,  
 DEFINITION complete cds.  
 ACCESSION AB094964  
 VERSION AB094964.1 GI:30172218  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 .  
 Asparagus officinalis (garden asparagus)  
 Asparagus officinalis  
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;  
 Asparagaceae; Asparagus.  
 1  
 Park, J., Ishikawa, Y., Yoshida, R., Kanno, A. and Kameya, T.  
 Expression of AODEF, a B-functional MADS-box gene, in stems and  
 inner tepals of dioecious species Asparagus officinalis L  
 Plant Mol. Biol. (2002) in press  
 2 (bases 1 to 952)  
 Kanno, A.  
 Direct Submission  
 Submitted (28-OCT-2002) Akira Kanno, Tohoku University, Graduate  
 School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi  
 980-8577, Japan (E-mail: kanno@ige.tohoku.ac.jp, tel: 81-22-217-5725,  
 Fax: 81-22-217-5725)  
 JOURNAL  
 AUTHORS  
 TITLE  
 REFERENCE  
 FEATURES  
 source  
 1. .952  
 /organism="Asparagus officinalis"





QY 374 ACCGAGAGAGATTAGAGAGAGAGAGAGATTGAGGCGATGACATTAAGC 433  
 DB 506 ATCTGAGAGAGAGATTAGAGAGAGAGAGAGATTGAGGCGATGACATTAAGC 565  
 QY 434 AACTGCGCGCTCTTGAAGAACTTTGGAAGAGTCTTTAGAAATTTGAGCATTAAGT 493  
 DB 566 AACTGCGCGCTCTTGAAGAACTTTGGAAGAGTCTTTAGAAATTTGAGCATTAAGT 625  
 QY 494 ATCATGATGCGCAGACAACTGACCTTAAGAAAGCTTAAGAAAGCAAGGAAA 553  
 DB 626 ATCATGATGCGCAGACAACTGACCTTAAGAAAGCTTAAGAAAGCTTAAGAAAG 585  
 QY 554 CTACCGCGCTCTTAATCATGAACTGATGATGAAAGAGAGATCCGAATCGGTTTA 613  
 DB 686 CACACCGGAATTAATGACAGAAATTTGAAATCTTTAGAGACCACTGATGAGGTTCC 745  
 QY 614 ATGTAGAAAACAGATGATTAATTAAGAAATTTGATTCATAGTGAAGAGTCTCTC 673  
 DB 746 ACG-----AGGATTCAAGCAATTAATGAGGCTGTTCTTCAAAATGACGGGCTC 799  
 QY 674 AGATGTTTCTCTTAAAGGTTGTCATCGAATCAGCCCAATCTGTTGTTAGTTATG 733  
 DB 800 ACATGATGCTCTTCGG---GTGCAACCCCAACCAAAATCTTCAAGAAACGGGATTA 856  
 QY 734 AATCAGATGATCTTAACTGCTTGCATTAAT 760  
 DB 857 GCTCTCAAGATCTTGGCTGCTTGAT 883

RESULT 6 980 bp mRNA linear PLN 09-AUG-2004  
 AY378150 Phalaenopsis equestris MADS box transcription factor (MADS3) mRNA.  
 LOCUS complete cds.  
 DEFINITION AY378150.1 GI:38680586  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Phalaenopsis equestris  
 Phalaenopsis equestris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 Epidendroideae; higher Epidendroideae; Vandae; Aeridinae;  
 Phalaenopsis.  
 1 (bases 1 to 980)  
 Tsai, W.C., Kuoh, C.S., Chuang, M.H., Chen, W.H. and Chen, H.H.  
 Four DEF-like MADS Box Genes Displayed Distinct Floral  
 Morphogenetic Roles in Phalaenopsis Orchid  
 Plant Cell Physiol. 45 (7), 831-844 (2004)  
 15295066  
 2 (bases 1 to 980)  
 Tsai, W.C., Chen, W.H. and Chen, H.H.  
 Direct Submission  
 Submitted (02-SEP-2003) Department of Biology, National Cheng Kung  
 University, 1 University Rd., Tainan, Taiwan 701, Republic of China  
 location/Qualifiers  
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ORIGIN  
 HBNLLRELETHAVVYVDDPNNYDGLALGNGASYLSFRTQSPQNLQGVYVPHD  
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 Query Match 34.5%; Score 316.8; DB 8; Length 980;  
 Best Local Similarity 65.3%; Pred. No. 1,5e-62;  
 Matches 503; Conservative 0; Mismatches 252; Indels 15; Gaps 2;

QY 65 GGAAGAGAGATGGGAGGGGAGATGAGATTAAGAAAGATGAGATCCAGCAAC 124  
 DB 185 GAAAGAGAACATGGGAGGGGAGATGAGATTAAGAAAGATGAGATCCAGCAAC 244  
 QY 125 GGAAGATTAATTTGAGAGAGAGTGGATCTGAAGAGCCAGAGAGCTCACTG 184  
 DB 245 GGAAGATTAATTTGAGAGAGAGTGGATCTGAAGAGCCAGAGAGCTCACTG 304  
 QY 185 TTCTGTGATGCTCAGGTCCTCTCATCATGTTCTCAAGACAGGAAAGTTGGTGA 244  
 DB 305 TTCTGTGATGCTCAGGTCCTCTCATCATGTTCTCAAGACAGGAAAGTTGGTGA 364  
 QY 245 ACTGACGCGCTCTACTGATTAATGAGGATTAATGAGGTCACAGTTGATCGGA 304  
 DB 365 ATTGATGCTTACACCGATACCAAGGTATATATGATCTTACACAGGTCGCGCA 424  
 QY 305 TGGATCTAGTAATGCTCAGTATGAGAGATGAGATGAGATAGCTGAAGCATCTGA 364  
 DB 425 TAAATTTATGAGCGAGCATGACGAGAGATGAGATGAGATGAGATGAGATGAG 484  
 QY 365 TTAACCAAACTGAGAGAGATTAAGAGAGAGAGAGAGAGATTTGAGGCGATG 424  
 DB 485 TAAACCAAACTGAGAGAGATTAAGAGAGAGAGAGAGAGATTTGAGGCGATG 544  
 QY 425 ACATTAAGCACTGCGGCTCTTGAAGAACTTTGAGAGTCTTTGAATTTGAGC 484  
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 QY 545 CAAGGAAACTTACCGGCTCTTAATCATGATGATGATGAAAGAGAGATCCGA 604  
 DB 665 CTCAAGAAACCAAGAGAACTTACTCGGAGAGCT-----GGAAGTACGACG 712  
 QY 605 ACGGTTTAATGTAAGAAACCAAGATTAATTAAGAAATTCATTCATGATGATG 664  
 DB 713 CCGTCTACTAGTGAAGATGATCCAAACTATGAGGCGCTTGAAGATGATG 772  
 QY 665 AGTGTCTCAGATGTTTCTTTAGGTTGTTCAATCCGAATGAGCCCAATCTGAG 724  
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 QY 725 TAGGTTAGATCATGATCTTACCTGATTAATGAGAGATTAATTAATTAATTA 784  
 DB 830 TTGATATGCTTCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 889  
 QY 785 GTATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 834  
 DB 890 CTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 939

RESULT 7 1005 bp mRNA linear PLN 09-MAY-2002  
 AB071378 Lilium regale LrDEF mRNA for MADS-box transcription factor,  
 LOCUS complete cds.  
 DEFINITION AB071378.1 GI:20513259  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Lilium regale  
 Lilium regale  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;

REFERENCE	1	Lilium.
AUTHORS	Winter, K. U., Weiser, C., Kaufmann, K., Bohne, A., Kitchner, C., Kanno, A., Saedler, H. and Theissen, G.	
TITLE	Evolution of class B floral homeotic proteins: obligate heterodimerization originated from homodimerization	
JOURNAL	Mol. Biol. Evol. 19 (5), 587-596 (2002)	
MEDLINE	21959322	
PMID	11961093	
REFERENCE	2 (bases 1 to 1005)	
AUTHORS	Kanno, A., Bohne, A., Saedler, H. and Theissen, G.	
TITLE	Direct Submision	
JOURNAL	Submitted (11-SEP-2001) Akira Kanno, Tohoku University, Graduate School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi 980-8577, Japan (E-mail: kanno@life.tohoku.ac.jp, Tel: 81-22-217-5725 (ex. 5725), Fax: 81-22-217-5725)	
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	/protein_id="BAB91550.1"	
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ORIGIN		
Query Match	33.2%; Score 304.2; DB 8; Length 1005;	
Best Local Similarity	68.0%; Pred. No. 1.2e-59;	
Matches	474; Conservative 0; Mismatches 208; Indels 15; Gaps 3;	
Db	72 AGAGATGGGAGGGGGAAGATGAGATAAAAAGATGAGATCCGAGCAAGCAAGT 131	
Db	6 AGTATGGGGGGGGAAGATGAGATTTAAGAAAGATCGAAAATCGAAGATCGACAGT 65	
Db	132 TACATATTTCTAAGAGAGAGATTGGGATCTGGAAGAGCCGAAAGCTCATCTTCTCTG 191	
Db	66 CACTTACTTCGAAGCCCGGACCGGAAATCATCAAGAGCGACTGAGCTCATCTGCTCTG 125	
Db	192 TGATGCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTACTGCGAG 251	
Db	126 TGATCCGAGGCTCTCTCTTATGTTCTTCAGCACCGGAAAGCTGTCAAGTTCTGAG 185	
Db	252 CCCCTCTACTGATATTAAAGGGGATATAGAGAGTACCAAGTTGTGACTGGAATGATCT 311	
Db	186 CCCCTCCACAAGCAGAAAGAGATCTTGACCGCTACCAAGCAGCTGTCCGGGATCAACT 245	
Db	312 ATGGAATGCTCAGTATGAGAGATCGAGATACGCTGAAAGCATCTGAAATGAGATTACCA 371	
Db	246 CTGGAGCCCGCAATCGAAGAAATCAAAACATTTGAAACCATCTGAGCGAGATCAACCG 305	
Db	372 AAACCTGAGGAAGGAGATTAGAGAGGAAGGAGGAGGAATTTGAGGGGATGGAATCAA 431	
Db	306 CAACCTCCGCAAGAGATCAGCAAGGATGGGGAGGAGCTGATGAGATTGGACATCAA 365	
Db	432 GCAATGCGCGGCTTTGAGCAAACTTTGGAAGATCTCTTGAATTTGTTAGGATAGAA 491	
Db	366 GGAAGCTGGCGGCTTTGAGCAAAATTTGAGCAGAGGCGCTCAAGCTCGTTTCGTCAGGA 425	
Db	492 GTATCATGTGATCGCAACAACCTGACATTTACAGAAAAAGCTTTAAAGACAGAGGA 551	
Db	426 GTATCATGTGATCAACCTGACAGCAGAGCTTTACAGAAAAAGCTTTAAAGACAGAGGA 485	

OY		552	AACCTTACCAGCGCTCAATTAATCATGAACTC-----GATTATGAAGAAGAGAAATCCGAA	602
Dd		486	AGCACACAAGAACTTGCTCCGTGGACTGTGGATAGAGATGATAAGATAGAAATCAACT	545
OY		603	CTACGGTTTAAATATGTAGAAAACACAGAGTAGAATTTATGAAAATTCATTCGAATGGTGAA	662
Dd		546	CTATGATT---ATGTAGACGAAGAACCCACGAACTATATGATGCGCGCTTCTCTGGCGAA	602
OY		663	TGAGTGTCTCCAGATGTGTTTCCCTTTAGGGTTGTTTCATCCGAATACGCCAATTCCTTGG	722
Dd		603	TGGGGCTTCTCATCTGTACGAACTCG---AGTCCAACCGAGCGACCAAACTGCATGG	659
OY		723	TTTAGGTATGAATCATCATGATCTTAAAGCTTGCAATA	759
Dd		660	GATGGGTATATGTTCTCCACGATCTCCGACTGACTTGA	696
RESULT_8				
AF503913				
LOCUS		AF503913	1039 bp	mRNA linear PLN 13-MAY-2000
DEFINITION		Lilium longiflorum MADS box protein (MADS1) mRNA, complete cds.		
ACCESSION		AF503913		
VERSION		AF503913.1	GI:20531752	
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
source				
gene				
CDS				
ORIGIN				
Query Match		32.6%	Score 289.4;	DB 8; Length 1039;
Best Local Similarity		67.6%;	Fed. No. 1.5e-58;	
Matches 471;		Conservative 0;	Mismatches 211;	Indels 15; Gaps 3
OY		72	AGAGATGGGAGGAGCGGAGATAGATATAAAAAGATAGAGAAATCCAGCAAGCGCAAGT	1311
Dd		12	AGCATTGGGGCGGGGAAAGATCGAATTTAAGAAGATCGAAGCTCGACGAATCGGCAAGT	71
OY		132	TACATATTCCTAAGAGAGAGATTGGGATCTGANAAGGCCAAGGAGCTCATCTGTTCTTG	191

Db 72 CACTTACTGGAAGCCGCGACCGGAATCATCAAGAAAGCACTGAGCTCATGTGCTCTG 131

Qy 192 TGATGCTCAGGTCCTCTCATCATGTTCTCAAGCAGAAAGTTGCTGATTAATGCGAG 251

Db 132 TGATGCGAAGTCTCTCTCTTATGTTCTCAGACACGGGAGAGCTGTCAGAGTTCTGAC 191

Qy 252 CCCCTCTCATGATTTAAGGGGATTTAGAGATCACAGTTGTGATCTGGAATGATCTT 311

Db 192 CCCCTCCACAGACAGAAAGATCTTCAGCCCTCACAGACCTGTCCGGATCAACCT 251

Qy 312 ATGAATGCTCAGTATGAGAGATGAGAAATGAGTAAAGCTGATCTGATGATTAACCA 371

Db 252 CTGAGAGCGCAATACAGAAATGCAAAACCTTGAACATCTGAGCGAGATCATCG 311

Qy 372 AAACCTGAGAGAGATTTAGAGAGAAAGGGGAGAAATGAGGGCATGACATTA 431

Db 312 CAACCTTCGAGAGAGATGACCGCAGAGATGGGGAGAGAGCTGATGATTTGACATCA 371

Qy 432 GCAACTGCGCGGCTTTAGCAAACTTTGAAAGATCTCTTGAATTTGTTAGGCATTA 491

Db 372 GGAAGCTGCGGCTTTAGCAAAATTTGACGAGAGCTCAAGCTCGTTGCTCACCGCA 431

Qy 492 GTATCATGTATGCGCACACAACTGACATTAAGAAAGCTTAAAGCAGCAAGGA 551

Db 432 GTATCATGTATCAACACTCAGACAGAGATTTACAGAAAGATCAAAACCTGCGA 491

Qy 552 AACTTACCGGCTCTAATAATCAATGAATG-----GATATGAAGAGAGAAATCCGA 602

Db 492 AGCACAAGAAAGCTGCTCGGTGACCTGTGAATCGAGAGATGAAGATGAGATTCAGT 551

Qy 603 CTACGCTTTTATGTAGAAAACAGAGTGAATTTAAGAAATTCATTCATGTGTGA 662

Db 552 CTATGCTT---ATGTGACGAGAAAGCCAGCACTATGATGCGGCTGTGCTGCGCA 608

Qy 663 TGAGTGTCTCAGATGTTTCTTTAGGGTGTTCATCCGAATCAGCCCAATCTGCTTG 722

Db 609 TGGGCTTCTCATCTGACAGATTCCG---AGTCCAAACCGAGCCAAACCTGCAATG 665

Qy 723 TTTAGTTATGAATCAGATGATCTTAGCTTCATTA 759

Db 666 GATGGTTATGCTCCCATGATCTCCGACTGCTTGA 702

RESULT 9 AF209729 833 bp mRNA linear PLAN 01-DEC-2000

LOCUS AF209729

DEFINITION Hemerocallis hybrid cultivar putative MADS box transcription factor (MADS1) mRNA, complete cds.

ACCESSION AF209729

VERSION AF209729.1 GI:11494136

KEYWORDS

SOURCE

ORGANISM Hemerocallis hybrid cultivar (daylily)

REFERENCE

AUTHORS Hemerocallis hybrid cultivar

TITLE Eukaryotic Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Hemerocallidaceae; Hemerocallis.

1 (bases 1 to 833)

2 (bases 1 to 833)

REFERENCE

AUTHORS Molecular changes during the expansion and senescence of ethylene-insensitive daylily flowers

TITLE Thesis (1999) University of California, Davis

2 (bases 1 to 833)

REFERENCE

AUTHORS Lange, N.E., Valpuesca, V., Napoli, C.A., Labavitch, J.M. and Reid, M.S.

TITLE Direct Submission

JOURNAL Submitted (30-NOV-1999) Environmental Horticulture, University of California, Davis, CA 95616-8587, USA

FEATURES

source

1..833

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/mol\_type="mRNA"

/cultivar="Cradle Song"

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ORIGIN

Query Match 32.2%; Score 295.6; DB 8; Length 833;

Best Local Similarity 66.9%; Pred. No. 1.2e-57;

Matches 459; Conservative 0; Mismatches 209; Indels 18; Gaps 2;

136 TATTCTAAGGAGAGTGGGATCTGAAGAGCCAGAGGCTCACTGTTCTCTGTAT 195

61 TACTCAAGAGAGGTGAGGTATCATGAGAAAGCCAAAGAACTCACTGTTCTGTAT 120

Qy 196 GCTCAGGTCCTCTCATCATGTTCTCAAGCAGAAAGTTGCTGATTAATCTGACGCC 255

Db 121 GCTGACCTGTCAATCATCATGTTCTGAGACCGGGAGAGTTCCGAGTATTCGAGCCC 180

Qy 256 TCTACTGATTTAAGGGATATATGAGAGTACCAAGTTGTGACTGGAATGATCTATG 315

Db 181 GGCATGACACGAAAGCGGTGTTGAGAGTATCAGAGCGACGACAGAAACTTGTG 240

Qy 316 AATGCTAGATATGAGAGATGAGATACCTGAGCATCTGATGATTAACCAAAAC 375

Db 241 AGTACACATATGAGAAATGCAAAACACTTGAATATCTCAAGAGATCAACATAT 300

Qy 376 CTGAGAGAGAGATTTAGAGAGAGAGAGAGAAATTTGAGGGCATGACATTAAGCAA 435

Db 301 TTGGCAGAGAAATTTAGCAGAGAGATTGAGAGAACTTATGATGATGATTTCAAGAA 360

Qy 436 CTGCGGCTTTTGAAGCAACTTTGGAAGTCTTTGAATTTGTTAGCATGAAGATAT 495

Db 361 CTGCGGCTTTTGAAGCAAAATCTGATGAAGCTTTGAAGTGTTCGCGTGAAGAAAT 420

Qy 496 CATGTGATCCGCACAAACTGACACTTACAGAAAGAAAGCTTAAAGCAGAGAAACT 555

Db 421 CATGTGATTAACCACTGACATGATCACTACAGAAAGAAAGTGAAGATTTCCAAAGAGCA 480

Qy 556 TACCGGCTCTAATACATGAATCTGATATGAAAGAGAGATCCGAATCAAGTTTAT 615

Db 481 CACAAGACTTTGCTGACAGAACTTGAAGAGCAAGTGA-----TGAATAT 525

Qy 616 GTAGAAAACAGATGAGATTTATGAATTCATTCATTCATTCATTCATTCATTCAT 675

Db 526 GCGATGAGAGACCGAGCACTATGATGATTCATTCATTCATTCATTCATTCATTCAT 585

Qy 676 ATGTTTCTTTAGAGTTGTTCAATCCGAATGAGCCCATCTGTTGTTTATGTTAGTAA 735

Db 586 ATGATGCTTACCG---AGTTCACCAAGCCAGCAACCTCCATGAGATGATGAG 642

Qy 736 TCATGATCTTACCTTGCATTAATG 761

Db 643 CCAATGATCTTCTGCTTGCATGATG 668

RESULT 10 AF230706 938 bp mRNA linear PLAN 02-JUN-2000

LOCUS AF230706

DEFINITION Tacca chantieri MADS box transcription factor AP3 mRNA, partial

ACCESSION	Cds.
VERSION	AP230706
KEYWORDS	AP230706.1 GI:8163953
SOURCE	Tacca chantieri
ORGANISM	Tacca chantieri Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae; Tacca.
REFERENCE	1 (bases 1 to 938) Kramer,E.M. and Irish,V.F. Evolution of the petal and stamen developmental programs: Evidence from comparative studies of the lower eudicots and basal angiosperms Int. J. Plant Sci. (2000) In press
JOURNAL	2 (bases 1 to 938)
AUTHORS	Kramer,E.M. and Irish,V.F.
TITLE	Direct Submission
JOURNAL	Submitted (03-FEB-2000) MCDB, Yale University, PO Box 208104, New Haven, CT 06511-8104, USA
FEATURES	Location/Qualifiers
source	1..938
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	<1..603
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	/codon_start=1
	/product="MADS box transcription factor Ap3"
	/protein_id="AAFP7935.1"
	/db_xref="GI:8163954"
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ORIGIN	
Query Match	31.9%; Score 292.8; DB 8; Length 938;
Best Local Similarity	67.9%; Pred. No. 5,1e-57;
Matches	440; Conservative 0; Mismatches 202; Indels 6; Gaps 2;
Dn	154 GGGATTCTGAAGAAGGCCCAAGAGCTCACTGTTCCTGTGATGCTCAGGTCTCTTCATC 213       4 GGATCATGMAAGAACCCAGAGAGCTCACCGTTCTTCGATCGTAGAGTTCTATCATC 63       214 ATGTTCTCAAGACAAGAAAGTTGGCTGATTACTGCAGCCCCCTACTGATTAAGAGG 273       Db 274 ATATATGAGAGGTACCAGGTTTGACTGATGATGATCTATGAAATGCTCAGTATGAGG 333 124 GTTTCGATCGGTTACACGAACTGACTGGATCGACTGTGAGTTCCGATGACGAGG 183       Qy 334 ATGCGAATACGCTGAAGCATCTGAATGATTAACCAAACCTGAGAGAGAGATTG 393 184 ATGCAAAATTAACCTGATCATCTGAGGAGATCAACCGAAATCTTGAAGGAAATTAAG 243       Db 394 AGGAGAAAGGGGAGGAATTTGAGGGGATGACATAAAGCAACGCGGGCTTGAGCA 453 244 CAAAGACCGGCGGAAGATTTTACGGCTTTGACATCAAGAACTCGTGCTTTGAGCA 303 454 ACTTTGAGAAGTCTCTTGAATTGTTAGCGATAGAAAGTATCATGTATGCGCCACACA 513 304 AATGTGAGATGAGGCTTTGAGATTGTTGTCTCAAGGAATATCATGTTATGACACACAG 363 514 ACTGACATTTACAGAAAAAGCTTAAAGCACAGGAACCTTACCGGCTTATATCAT 573 Db 364 ACCGATACATATTAAGAAAGAGCTGAAGATTCCATGAAGCTCACAGGAACCTATGGA 423 574 GAACGTGATATGAAAAGAGGAATCCGAATCAACGGTTTTTAATGTGAAAACAGAGTGA 633 424 GAACGTGAGATGAGATGAGACCCGATTTTACGGGTTT---GTCGACATGATCTTCTCT 480

QY	634	ATTATGCAAAATTCGATTCCTCAATGGGAAAGAGAGTCCTCAAGATGTTTCTTTAGAGGT	693
DB	481	AACACACACAGCGCTCTGGCACTGGCAAAATGCTGGGCTTCATGTCACGGCTACCG--T	537
QY	694	GTTTCATCCGAATCAGCCCAATCTGCTTGTTAGTTAGTTATGAATACATGATCTTAGGCTT	753
DB	538	GTTTCAGCCAAAGCCAGCCAAATCTTCATGAAATGAGGATGACAGTTCTCATGACCTTCGCTG	597
QY	754	GCATTAATGACAGTAATATTATGATTTTATTGATTTTATTTTATGT	801
DB	598	GCATGAACACATGCGTGGAAGCTGGCTTTCCTTTGATGCTGATGTTGT	645
RESULT 11			
AY337750	651 bp	mRNA	linear
LOCUS	AY337750	Eupomatia bennettii APETALA3-like protein Ap3-1 mRNA, complete cds.	PLN 31-JUL-2004
DEFINITION	AY337750		
ACCESSION	AY337750.1	GI:37993050	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
CDS			
ORIGIN			
Query Match	31.1%;	Score 285.4;	DB 8; Length 651;
Best Local Similarity	68.4%;	Pred. No. 2.6e-55;	
Matches 410;	Conservative 0;	Mismatches 186;	Indels 3; Gaps 1;
QY	76	ATGGGGAGGGGGAAGATGAGATTAATAAAGATGAGATCCGACGAACAGGCAAGTTACA	135
DB	1	ATGGGGAGAGGAAGATCGAGATTAATAAAGATGAGATTCACCTAACAGCAAGTACT	60
QY	136	TATTTCAAGGAGAGTGGGATCTGGAAGAAGCCCAAGAGCTCAGTGTCTCTGAT	195
DB	61	TACTCGAAGGAGAGGATGATTAATGAAGAACTAAGAGGCTTACTGTCTTGGCAT	120
QY	196	GCTCAGGCTCTCATCATGTTTCTCAAGACAGAAAGTTGGCTGATTACTGACAGCCC	255
DB	121	GCTAGGTTCTCTTATTATGTTCTCCAAATCTGCAAGTTCTCGAATCTGAGCCCT	180
QY	256	TCTACTGATATTAAGGGATATATGAGAGGTACAGGTTGTGACTGGAATGATCTATGG	315
DB	181	TCTCAACAGACTAAGAGATTTTGCATCTTACAGGAAGTTTCACACCAACTTGTGG	240
QY	316	AATGCTCAGATGAGAGATTCAGAAATACGCTGAGATCTGGAATGAGATTACCAAAAC	375

Db 241 AATTCTGATTACGAGAAATGCAAGCTCACTTGAAACAACTCAAGAGATAATTAACAT 300  
 Qy 376 CTGAGGAAGAGATTAGGAGAGAGAGGAGGAATTGGAAGCATGACATTAAGCAA 435  
 Db 301 CTCGGAGGAGATCAGCAAGAAAGATTGTGAAGATCTGGAAGATCTAGAATGAGAG 360  
 Qy 436 CTGCGCGGTCTTGAGCAACTTTGGAAGAGTCTTTGAATTTGTAGCATGAANAATAT 495  
 Db 361 CTGCGCGGTCTTGAGCAAAATCTGAGCAATTTCTAATCAAAATTTGTTCTGAGAGAAATAT 420  
 Qy 496 CATGTATGCGCACACAACTGACCTTAACAAGAAAGCTTAAGACAAAGGAAACT 555  
 Db 421 CATGTATGCGCACTCAAACTGAGCTTTCAGAGAAAGCTGAGAACTTGACAGAAACA 480  
 Qy 556 TACCGCGCTCTAATACATGAACTGATATGAAAGAGAGATCCGAATCGGTTTAAAT 615  
 Db 481 CATGACAGTTTAGTACGTCGATTTGGAAGACAGCTGAGATGGGGATATGGTT---G 537  
 Qy 616 GTAGAAAACAGAGTAGAATTATGAAATTCGATTCGAATGGTGAATGATGTCCTCA 674  
 Db 538 GTGATGATGATGGTGCCAGACTATGAAATCTGCACTTGTGGCCAAATGGTGTGCTCA 596

## RESULT 12

AY337751 651 bp mRNA linear PLN 31-JUL-2004  
 LOCUS Apomastia bennettii APETAUA3-like protein AP3-2 mRNA, complete cds.  
 DEFINITION AY337751  
 ACCESSION AY337751  
 VERSION AY337751.1 GI:37993052  
 KEYWORDS  
 SOURCE Apomastia bennettii  
 ORGANISM Apomastia bennettii  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; magnoliids; Magnoliales;  
 Eupomatiaceae; Eupomatia.

REFERENCE 1 (bases 1 to 651)  
 Kim, S., Soltis, D.E. and Soltis, P.S.  
 Pre-angiosperm duplication of floral genes and regulatory tinkering  
 at the base of flowering plants  
 Unpublished

JOURNAL 2 (bases 1 to 651)  
 Kim, S., Soltis, D.E. and Soltis, P.S.  
 Direct Submission  
 Submitted (09-JUL-2003) Dept. of Botany, University of Florida,  
 P.O. Box 118526, Gainesville, FL 32611, USA  
 location/Qualifiers  
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ORIGIN  
 Query Match 31.1%; Score 285.4; DB 8; Length 651;  
 Best Local Similarity 68.4%; Pred. No. 2.6e-55;  
 Matches 410; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

Qy 76 ATGGGAGGGGGAAGATGAGATAAAGATAGAGATCCGACGAAGCAAGTCA 135  
 Db 1 ATGGGAGAGGAAAGATGAGATAAAGATAGAGATCCGACGAAGTCA 60  
 Qy 136 TATTTAAGAGAGAGATTGAGTACTGAAGAGGCAAGAGCTCACTGTTCTGTGAT 195  
 Db 61 TACTGGAAGAGAGGATGATTTAGAGAAAGCTTAAGAGACTTCTGTTCTCGCAT 120

Qy 196 GCTCAGGTCTCTCATCATGTTCTCAGACAGAAAGTGGCTGATTACTGACCCC 255  
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 Qy 256 TCTACTGATTTTAAAGGGATATATGAGAGTACAGAGTTTGACTGAAATGATCTATGG 315  
 Db 181 TCTACAGAGCTAAGAAAGATTTTCATCGTTTACAGAAAGTTTCAAGACCAACTGTGG 240  
 Qy 316 AATGCTAGATAGAGAGATGCAAAATACCTGAGCATTTGAATGATTAACCAAAAC 375  
 Db 241 AATTCTCATTCAGAAAGAAATGCAAGCTCACTTGAACAAATCTCAAGAGATAATTAACAT 300  
 Qy 376 CTGAGGAAGAGATTAGGAGAGAGAGGAGGAATTTGAGGCGCATGACATTAAGCAA 435  
 Db 301 CTCGGAGGAGATCAGGCAAGAAATTTGAAAGTCTGAAAGATCTAGAAATGAGAG 360  
 Qy 436 CTGCGCGGTCTTGAGCAAACTTTGGAAGAGTCTTTGAATTTGTAGCATGAANAATAT 495  
 Db 361 CTGCGCGGTCTTGAGCAAAATCTGAGAGATTTATCAAAATTTGTTGTGAGAGAAATAT 420  
 Qy 496 CATGTATGCGCACACAACTGACACTTACAGAGAAAGCTTAAAGCACAGGAAACT 555  
 Db 421 CATGTATGCGCACTCAAACTGAGACTTACAGAGAAAGCTGAGAACTTGACAGCA 480  
 Qy 556 TACCGCGCTCTAATACATGAACTGATATGAAAGAGAGAAATCCGAATCGGTTTAAAT 615  
 Db 481 CATGACAGTTTAGTACGTCGATTTGGAAGACAGAGATGGGGATATGGTT---G 537  
 Qy 616 GTAGAAAACAGAGTAGAATTATGAAATTCGATTCGAATGGTGAATGATGTCCTCA 674  
 Db 538 GTGATGATGATGGTGCCAGACTATGAAATCTGCACTTGTGGCCAAATGGTGTGCTCA 596

## RESULT 13

AB050649 852 bp mRNA linear PLN 31-OCT-2001  
 LOCUS Magnolia praecocissima mRNA for putative MADS-domain transcription  
 factor MpMADS7, complete cds.  
 DEFINITION AB050649  
 ACCESSION AB050649  
 VERSION AB050649.1 GI:16549069  
 KEYWORDS  
 SOURCE Magnolia praecocissima  
 ORGANISM Magnolia praecocissima  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; magnoliids; Magnoliales;  
 Magnoliaceae; Magnolia.

REFERENCE 1  
 Ito, M., Shibata, S., Tanabe, Y. and Hasebe, M.  
 Organ identities in Magnolian flower  
 Unpublished

JOURNAL 2 (bases 1 to 852)  
 Ito, M., Shibata, S. and Hasebe, M.  
 Direct Submission  
 Submitted (31-OCT-2000) Motoomi Ito, University of Tokyo, Department  
 of Systems Sciences, Graduate School of Arts and Sciences, 3-8-1  
 Komaba, Meguro-ku, Tokyo 153-8902, Japan  
 E-mail: cmico@mail.ecc.u-tokyo.ac.jp, Tel: 81-3-5454-6638,  
 Fax: 81-3-5454-6638  
 location/Qualifiers  
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 /db\_xref="taxon:81865"  
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## ORIGIN

Query Match 31.1%; Score 284.8; DB 8; Length 852;  
Best Local Similarity 70.7%; Pred. No. 3.ee-55;  
Matches 379; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY ATGGGAGGGGGAAGATAGATATAAAGATAGAGATCCGACGAACAGCAAGTTACA 135  
DB ATGGGAAGAGGGAAGATAGAGATATAAAGATAGAGATCCGACGAACAGTTACA 60  
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DB TATTTCAAGAGAGAGTGGGATCTGAAGAGCCAGAGAGCTCACTGTTCTGTGAT 120  
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DB GCTCAGAGTCTCTCATCATGTTCTCAAGACAGGAAGTGGCTGATTACTGACAGCCC 180  
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DB TCTACAACCAAGAAATATTTTGCATCGTTACAGACAGCTTCGGGATCAGCTTATG 240  
QY AATGCTCATGATAGAGAGATGCGATATCGCTGAGATCTGAATGAGATTAAACCAAC 375  
DB AATCTCATCACTACAGAGAAATGCAAGCACTGATCAATCTCAAGAGAAATTAACAT 300  
QY CTGAGGAAGAGATTGAGAGAGAGAGGGGAGGAATTGAGGGCAATGACATTAAGCA 435  
DB CTCCGAGGGAATTCAGGCAAGAGATCGGAAAGATCTGGAAGATCTGGAATCGAAGA 360  
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DB CTGCGGGCTTTGAGCAAACTTTGGAAGAGTCTTTGAATGTTAGGCAATGAATAT 420  
QY CATGTGATGCCCAACAACCTGACCTTACAGAAAAAGCTTTAAAGCACAAGGAAT 555  
DB CATGTGATGCCCAACAACCTGACCTTACAGAAAAAGCTTTGAGAGCTTGCAGATGA 480  
QY TACCGGCTCTATATACATGAACTGATATGAAGAGAGAAATCGGAGCTT 611  
DB CACGCAAAATTAATTGCTCATTTGAGAGGTCAGAGCTGAGAACGGGCTTACGGCTT 536

RESULT 14 830 bp mRNA linear PLN 21-AUG-2004  
AY621154  
LOCUS  
DEFINITION Alpina hainanensis AP3-like MADS-box protein (MADS) mRNA, partial  
cds.  
ACCESSION AY621154 GI:51243293  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Alpina hainanensis  
Alpina hainanensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales;  
Zingiberaceae; Alpina.  
1 (bases 1 to 830)  
Song,J.J., Ma,W., Liao,J.P. and Tang,Y.J.  
Characterization of class B and C floral organ gene from Alpina  
hainanensis  
Unpublished

REFERENCE  
AUTHORS  
TITLE

JOURNAL  
REFERENCE  
AUTHORS  
TITLE

JOURNAL  
REFERENCE  
AUTHORS  
TITLE

FEATURES  
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## CDS

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EKMDHGYMTVDDGVFAHMYSYKQVPPNPNDLIRSYASHHDLRLA"

## ORIGIN

Query Match 30.8%; Score 282.6; DB 8; Length 830;  
Best Local Similarity 73.0%; Pred. No. 1.2e-54;  
Matches 363; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY AAAAGATAGAGATCCGACGAACAGCAAGTTACATATTCTAAGAGAGAGTTGGATAC 160  
DB AGAAGATAGAGAACCAACCAACAGGAGAGTGAATTAATCAAGAGAGTGAAGATCA 61  
QY TGAAGAGCCCAAGAGCTCACTGTTCTGTGATGCTCAGGTTCTCTCATCATGTTCT 220  
DB TGAAGAGCCCAAGAGCTCACTGTTCTGTGATGCTCAGGTTCTCTCATCATGTTCT 121  
QY CAAACAGAGAAAGTTGGCTGATTAAGTCAAGCCCTCTACTGATATTAAAGGGATATATG 280  
DB CCAAGCAGGCAAGTTCTGATTAAGTCAAGCCCTCTACTGATATTAAAGGGATATATG 181  
QY AGAGTACCAAGTGTGACTGGAATGATCTATGGAATGCTCAATGAGAGATGACAGA 340  
DB AGGTTATCAACAAAGTGTGACTGGAATGATCTATGGAATGCTCAATGAGAGATGACAA 241  
QY ATACGCTGAAGCATCTGAATGATTAACCAAACTGAGGAAGAGATTAAGAGAGAGA 400  
DB ATATATGAAACGCTTCAAGAGATCAACCGTAAATCCGAGAGAAATTAAGAGAGAGA 301  
QY AGGGAGAGAAATGAGGGCATGACATTAAGCAACTGCGCGGCTTTGAGCAAACTTTGG 460  
DB TGGGTAAAGTCTCGATGAGATGACATTAAGCAACTGCGCGGCTTTGAGCAAACTTTGG 361  
QY AAGAGTCTCTTAAGATTTGAGCATGAGAAAGTATCATGTATCGCCACACAACTGACA 520  
DB ATGAGGCATTTAAAGTTGTTGCAATGAGAAATATCATGTATGACACTCAACACAGAGA 421  
QY CTTAACAAGAAAAAGCTTAAGCAAGAGAACTTAACCGCGCTCTAATATCATGAACTGG 580  
DB CTTAACAAGAAAAAGCTTAAGCAAGAGAGCTCCCAAGAAAGCTCAAGAAATTAATCAATTTG 481  
QY ATATGAAGAGAGAAAT 597  
DB AGATGAAGATGAACAT 498

RESULT 15 1002 bp mRNA linear PLN 31-OCT-2003  
AB094965  
LOCUS  
DEFINITION Tulipa gesneriana TGBEFA mRNA for MADS-box transcription factor,  
complete cds.  
ACCESSION AB094965  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Tulipa gesneriana  
Tulipa gesneriana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;  
Tulipa.

Tulipa gesneriana  
Tulipa gesneriana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;  
Tulipa.

FEATURES  
source  
1..830

REFERENCE  
AUTHORS 1 Kanno, A., Saeaki, H., Kamaya, T., Saedler, H. and Theissen, G.  
TITLE heterotopic expression of class B floral homeotic genes supports a  
modified ABC model for tulip (*Tulipa gesneriana*)  
JOURNAL Plant Mol. Biol. 52 (4), 831-841 (2003)  
PUBMED 22856392  
PUBMED 13677470  
REFERENCE 2 (bases 1 to 1002)  
AUTHORS Kanno, A.  
TITLE Direct Submission  
JOURNAL Submitted (28-OCT-2002) Akira Kanno, Tohoku University, Graduate  
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi  
980-8577, Japan (E-mail: kanno@life.tohoku.ac.jp, Tel: 81-22-217-5725,  
Fax: 81-22-217-5725)  
FEATURES  
source Location/Qualifiers

1. 1002  
/organism="Tulipa gesneriana"  
/mol\_type="mRNA"  
/cultivar="White Dream"  
/db\_xref="taxon:13306"  
/feature\_type="flower"  
1. 1002  
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72. 758  
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/translation="MGRKTIKIKIENSTKROVYSRBSGIMKANELTVLCDAEVS  
LMPFSSTHKLSEFSESTNOKKIDRYQMTGIMLSAQYKQNTFNHLSQIRNLR  
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GYGHLRLRLA"

## ORIGIN

Query Match 30.8%; Score 282.2; DB 8; Length 1002;  
Best Local Similarity 65.6%; Pred. No. 1.4e-54;  
Matches 464; Conservative 0; Mismatches 228; Indels 15; Gaps 3;

QY 76 ATGGGAGGGGAGATAGATATAAAGATAGAGATCCGACAGCAAGGATTACA 135  
DB 72 ATGGGTCGTGGCAAGATCGAATCGAAGATCGAATCAACCAACCGTCAGGTCACT 131  
QY 136 TATTCTAAGAGAGAGTGGATATCTGAAGAAGGCCAAGAGCTCACTGTTCTCTGTGAT 195  
DB 132 TATTCAAGCTCCGACAGTGGATCATGAAGAAGGCCAAGACTCAGTCTCTTGGCAT 191  
QY 196 GCTCAGGTCCTCTCATCATGTTCTCAAGCAAGGAAGTTGGCTGATTACTGCAAGCCCC 255  
DB 192 GCTGAAGTTTCCCTACTCATGTTTCAAGCACTCAAGACTCTCCGAGTCTGCAAGTGA 251  
QY 256 TCTACTGATATTAAAGGGATATATGAGAGGTAACCAAGTGTGACTGGAATGATCTATG 315  
DB 252 TCCACCAATCGAAGAAAGATCTTCGACCGGTACCAAGATGACTGGAGTCAACTTGG 311  
QY 316 AATGCTCAGTATGAGAGATCGAATACGCTGAAGCATCTGAATGATTAACCAAAAC 375  
DB 312 AGCGGCAATACGAGAAATGCAAGATACGTTCAACCATCTGAGCCAGATCAACCGTAA 371  
QY 376 CTGAGGAAGAGATTAGAGAGGAAGAGGGGAGGAATTGAGAGGCGATGACATAAGCAA 435  
DB 372 CTTCGACAGGAGATTAAGCAAGAGATGGGGAGAGCTGATGCTGGAATTCAGCGAG 431  
QY 436 CTGCGCGGCTTGGAGCAAACTTGGAGAAGTCTCTTAAGATTGTAAGCATGAAGTAT 495  
DB 432 CTGCGCGGCTTGGAGCAAAATTTGAGAGAGGCTTTGAAGATTGTTGCGGAGGAAGTAT 491  
QY 496 CATGTGATCGCCACAACTGACACTTAACAAGAAAAGCTTAAAGCAACAAGGAAACT 555  
DB 492 CATGTGATTTGTAATCAAGACAAACCTACAGAAAAGGTGAAAATTCGAGAGAACT 551  
QY 556 TACCGCGCTTAATAATGAACTG-----GATATGAAGAAGAGAAATCCGAATAC 606

DB 552 AATAAGAACTTGCTCCGAGACCTGTGGAACATAGAGATGAAAGATGAGCATCAAGCTTAC 611  
QY 607 GGTATTAATGTAAGAAAACCAAGATGAATTTTGAATAATTCATTCATATGATGATG 666  
DB 612 GGTATATATAGAGATGACCCGAAACAG--CTATAGAGGAGGCGCTTCTGCGAATG 668  
QY 667 TGTCTCAAGATGTTTCTTTAGGGTGTTCATCCGATCAGGCCAATCTGCTGGTTTA 726  
DB 669 GGAATTAAGATGACAGATTCG--GATCAACCAAGCCAAACCTCCAGGGGATG 725  
QY 727 GGTATGAATCAATGATCTTAGCCCTTGATATAGAGAGATATAT 773  
DB 726 GGTATGACTCATGATCTTGGCTTGTGTAACCTCGAATCTT 772

Search completed: October 6, 2005, 11:40:40  
Job time : 4378 secs

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RESULT 4
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ID ADJ44530 standard; cDNA; 681 BP.
XX
AC ADJ44530;
XX
DT 06-MAY-2004 (first entry)
XX
DE Plant cDNA #5530.
XX
KM Plant; gene; ss; transcription; plant genome augmentation; cereal;
KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KM stress tolerance; salt tolerance; drought tolerance;
KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KM antifungal.
XX
OS Eukaryota.
XX
PN US2004016025-A1.
XX
PD 22-JAN-2004.
XX
PF 26-SEP-2002; 2002US-00260238.
XX
PR 26-SEP-2001; 2001US-0325277P.
PR 26-SEP-2001; 2001US-0325448P.
PR 04-APR-2002; 2002US-0370620P.
XX
PA (BUDW/) BUDWORTH P.
PA (MOUN/) MOUNHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREBS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
XX
PI Budworth P, Mounhamer T, Briggs SP, Cooper B, Glazebrook J;
PI Goff SA, Katagiri F, Krebs J, Provart N, Rique D, Zhu T;
XX
DR WPI; 2004-190374/18.
XX
PT New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.
XX
PS Example 13; SEQ ID NO 5530; 230bp; English.
XX
CC The invention relates to plant nucleotide sequences that direct seed-,
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

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XX
SQ Sequence 681 BP; 156 A; 213 C; 215 G; 97 T; 0 U; 0 Other;
XX
Query Match 25 6%; Score 234.8; DB 12; Length 681;
Best Local Similarity 65.8%; Pred. No. 3.7e-50;
Matches 341; Conservative 0; Mismatches 177; Indels 0; Gaps 0;
XX
QY 76 ATGGGAGGGGGAAGATAGATTAATAAAGATAGAGAAATCCGACGACGAGGAGTTACA 135
DB 1 ATGGGGCGGGGCAAGATCGAGATCAAGCGGAGTCGAAAGCCACCAACCGCAGGTGACC 60
QY 136 TATTTAAGAGAGAGTTGGATTAAGTAAAGAGCCAGAGCTCATCTTTCTGTGAT 195
DB 61 TACTCCAAACCGCCGACGGGGATCATGAAGAGGCGCGAGACTACCTGTCTGCGAC 120
QY 196 GCTCAGAGTCTCTCTCATCTGTTTCAACACAGAGAAAGTTGGCTTACTGACGCCCC 255
DB 121 GCCCAGGTGCGCATCATGTTCTTCACCCGGCAAGTACACGAGTTGCGAGCCCC 180
QY 256 TCTACTGATATTAAAGGGGATATATAGAGAGTACCAAGTTGTGACTGAAATGATCATG 315
DB 181 GGAACCGACATCAAGACCATCTTTGACCGGTACACGACGCAATCGGACCAAGCCTATG 240
QY 316 AATGCTCAGTATGAGAGATGCAAGATACGCTGAAGCATCTGAATGAGATTAAACAAAC 375
DB 241 ATGAGCAGATATGAGAAATATGACAGCGCAGCTGAGCATCTCAAGACATCATCGTGT 300
QY 376 CTGAGGAAGAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435
DB 301 CTGCGACAGAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 436 CTGCGGCTCTTGAGCAAACTTGGAGAGAGTCTCTTGAATTTGATAGCATGAAGATAT 495
DB 361 CTGCGGCGCTCTGAGAGAAACGTCAGCGGGCTCTCAAGAGAGTTGCGCATGGAAGTAC 420
QY 496 CATGTATGCGCACACAAACTGACACTTACAAAGAAAAGCTTAAAGCAAGGAAACT 555
DB 421 CATGTATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 480
QY 556 TACCGGCTCTTATACATGAACGTGATGAAGAGGA 593
DB 481 TACAGAACCTGACGAGAGGCTAAGGCAATGCGGAGGA 518
XX
RESULT 5
AAF85392
ID AAF85392 standard; cDNA; 946 BP.
XX
AC AAF85392;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of the floral homeotic protein PTD.
XX
KM Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;
KM LFY; FLORICULA; FLO; DEFICIENS; DBF; AGAMOUS; AG; transgenic plant;
KM fertility; sterility; ss.
XX
OS Populus balsamifera.
XX
FH Key Location/Qualifiers
FH CDS 1..684
FT /tag= a
FT /product= "PTD"
XX
PN CA2319853-A1.
XX
PD 01-APR-2001.
XX
PF 02-OCT-2000; 2000CA-02319853.
XX
PR 01-OCT-1999; 99US-00410464.
XX

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Best Local Similarity 58.3%; Pred. No. 2,3e-48;  
Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

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Qy 76 ATGGGAGGGGGAAGATGAGTAAAGATGAGATCCGAGCAAGCAAGTTACA 135
Db 1 ATGGGAGGGGGAAGATGAGTAAAGATGAGATCCGAGCAAGCAAGTTACA 60
Qy 136 TATTCTAAGAGAGTGGGATCTGTAAGAGGCCAAGAGCTCATGTTCTCTGAT 195
Db 61 TACTCGAAGAGAAATGATTTTCAAGAAAGCCCAAGAACTCAGTACTTGTGAT 120
Qy 196 GCTCAGGCTCTCTCATCATGTTCTCAAGCAAGAAAGTGGCTGATTAATGAGCCCC 255
Db 121 GCTAAGGCTCTCTCATCATGTTCTCAAGCAAGAACTCAGTACTTGTGAT 180
Qy 256 TCTACTGATATTAAAGGGAATATGAGAGTACCAAGTTGACTGGAATGATCTATGG 315
Db 181 TCCACATCGACAAAGAAATCTACGATCAATATCAGAACCTTTAGGCGATATGTTGG 240
Qy 316 AATGCTGATATGAGAGATGAGATACGCTGAGAGATCTGATGATTAACCAAAAC 375
Db 241 GGCACTCAATACGAAATGCAAGACACTTGGAAAGCTGAAATGATATCATATAG 300
Qy 376 CTGAGAAAGAGATTAGAGAGAGAGAGAGAGGAGATTTGAGGGCATGACATTAAGCAA 435
Db 301 CTGAGACAAAGAAATCAGGCAAGAGAGAGAGAGGCGCTGATGATCTGAGCATTTGATCAT 360
Qy 436 CTGGCGGCTCTTGAAGCAACTTTGGAAGAGTCTTTGAAATTTGTTAGGCATTAAGATAT 495
Db 361 CTGGCGGCTCTTGAAGCAACTATGATGAAAGCCCTTGAATGGTGTGCTGGCAGGAAGTAC 420
Qy 496 CATGTGATGCGCACAACTGACACTTAACAAGAAAGCTTAAAGCACAGGGAAGT 555
Db 421 CATGTGATCAAAACAAACAAACAAACCTTACAGAAAGGTTGAAGATTGAGAGAGAGA 480
Qy 556 TACCGCGCTCTTAATATACATGAACTGATATGAAAGAGAGAACTCCGAACTACGGTTTAT 615
Db 481 CATGGAAGACCTCTGATGAAATATGAAAGCAAAATAGAGGATTCAGATATGTTAGTG 540
Qy 616 GTAGAAAACAGAGATGAAATTTATGAAATTCGATTCGATGATGATGATCTCTCAG 675
Db 541 GACAAATAGAGCTGCTGTGCACTTGCAAAATGGGCTTCCAACTCTATGATTCGCGCTG 600
Qy 676 ATGTTTCTTTAGGGTGTTCATCCGATCAGCCCAATCGTGGTTAGGTTATGAA 735
Db 601 CATACGGGCAACACACACACATCTCCCTAATCTTCACTTGAAGATGATTTGGA 660
Qy 736 TCACTGATCTTAGCCTTGATTA 759
Db 661 GCCCATGAACTTGGCTTCTTGA 684

```

RESULT 7  
ACA62518  
ID ACA62518 standard; cDNA; 946 BP.

XX ACA62518;  
XX 18-AUG-2003 (first entry)  
XX Poplar homeotic gene PTD, cDNA.  
XX DE  
XX Poplar; ss; gene; PTD; deficiency; homeotic gene; floral development;  
XX KW sterile tree; pulp; paper; plant.  
XX OS  
XX Populus balsamifera subsp. trichocarpa.  
FH Key  
FT CDS  
FT 1.684  
FT /tag= a  
FT /product= "PTD"  
FT /note= "This CDS is specifically claimed in claim 1"

PN US2003033628-A1.

XX 13-FEB-2003.

XX 21-MAR-2002; 2002US-00104580.

XX 06-APR-1998; 98US-0080851P.

XX 06-APR-1999; 99US-00287700.

XX 01-OCT-1999; 99US-00410464.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Straus SH, Rotmann W, Brunner A, Shepard L;

XX WPI; 2003-466273/44.

XX DR P-PSDB; ABU61893.

XX PT

XX Claim 1; Page 20-21; 48pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising at least 15 consecutive nucleotides of the gene, cDNA or coding sequence of 4 homeotic genes from poplar, PTLF (LEAFY and FLORICA homologue), PTD (DEFICIENS homologue), and PTAG-1/PTAG-2 (both homologues of AGAMOUS).

XX Also included are a recombinant nucleic acid molecule comprising a cell promoter sequence operably linked to the nucleic acid molecule, a cell transformed with the nucleic acid molecule, a transgenic plant comprising the recombinant nucleic acid molecule and the purified proteins encoded by the nucleic acids. The nucleic acid molecules are useful for the manipulation of flowering in poplar and other plant species, for producing transgenic plants having modified fertility characteristics (particularly sterility) and in the pulp and paper industries. The present sequence is the poplar PTD cDNA

XX Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

XX Query Match 24.9%; Score 228; DB 9; Length 946;

XX Best Local Similarity 58.3%; Pred. No. 2,3e-48;  
Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

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Qy 76 ATGGGAGGGGGAAGATGAGTAAAGATGAGATCCGAGCAAGCAAGTTACA 135
Db 1 ATGGGAGGGGGAAGATGAGTAAAGATGAGATCCGAGCAAGCAAGTTACA 60
Qy 136 TATTCTAAGAGAGTGGGATCTGTAAGAGGCCAAGAGCTCATGTTCTCTGAT 195
Db 61 TACTCGAAGAGAAATGATTTTCAAGAAAGCCCAAGAACTCAGTACTTGTGAT 120
Qy 196 GCTCAGGCTCTCTCATCATGTTCTCAAGCAAGAAAGTGGCTGATTAATGAGCCCC 255
Db 121 GCTAAGGCTCTCTCATCATGTTCTCAAGCAAGAACTCAGTACTTGTGAT 180
Qy 256 TCTACTGATATTAAAGGGAATATGAGAGTACCAAGTTGACTGGAATGATGATG 315
Db 181 TCCACATCGACAAAGAAATCTACGATCAATATCAGAACCTTTAGGCGATATGTTGG 240
Qy 316 AATGCTGATATGAGAGATGAGATACGCTGAGAGATCTGATGATTAACCAAAAC 375
Db 241 GGCACTCAATACGAAATGCAAGACACTTGAAGAGCTGATATGATTAATGATTAAG 300
Qy 376 CTGAGAAAGAGATTGAGAGAGAGAGAGAGGAGAAATGAGGCGCATTAAGCAA 435
Db 301 CTGAGACAAAGAAATCAGGCAAGAGAGAGAGGCGCTGAATGATCTGAGCATTTGAT 360
Qy 436 CTGGCGGCTCTTGAAGCAACTTTGGAAGAGTCTTTGAAATTTGTTAGGCATTAAGAT 495
Db 361 CTGGCGGCTCTTGAAGCAACTATGATGAAAGCCCTTGAATGGTGTGCTGGCAGGAAGTAC 420
Qy 496 CATGTGATGCGCACAACTGACACTTAACAAGAAAGCTTAAAGCACAGGGAAGT 555

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Db 421 CATGTGATCAAAACAAAACGAAACCTTACAGAGAGAGATTTAGAGAGAGA 480  
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Qy 616 GTAGAAAACCAAGTGAATTTATGAAAATTCGATTCCGATGGTGAATGAGTGTCTCAG 675  
Db 541 GACAAATGAAAGCTGCTGTGCACTTGCAAAATGGGGCTTCCAACTCTATGCAATCCGCTG 600  
Qy 676 ATGTTTTCCTTGAAGGTTGTTCAATCCGATCAGCCCAATCGCTGTTAGGTTATGAA 735  
Db 601 CATCAGGGGACAAACCAACCAACATCTCTTAATCTTCACTTGAAGATGATTTGA 660  
Qy 736 TCACATGATCTTAGCCCTTGATTA 759  
Db 661 GCCCATGAACTTGCCCTTCTTGA 684

RESULT 8  
AAF85393 standard; cDNA; 681 BP.  
AAF85393;  
AAAF85393;  
23-JUL-2001 (first entry)  
Nucleotide sequence of the floral homeotic protein PTD.  
DE Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;  
KM LFY; FLOXICANLA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;  
fertility; sterility; ss.  
XX  
OS Populus balsamifera.  
XX  
XX Key Location/Qualifiers  
FH 1. .681  
FT CDS /\*tag= a  
FT /product= "PTD"  
XX  
PN CA2319853-A1.  
XX  
PD 01-APR-2001.  
XX  
PF 02-OCT-2000; 2000CA-02319853.  
XX  
PR 01-OCT-1999; 99US-00410464.  
XX  
PA (UYOR-) UNIV OREGON HEALTH SCI.  
XX  
PI Roctman WH, Strause SH, Brunner AM, Sheppard LA;  
XX  
XX WPI; 2001-336098/36.  
XX  
XX P-PSDB; AAB868435.  
XX  
XX Novel isolated polynucleotide derived from Populus species, useful for  
PT producing transgenic plants having modified fertility characteristic,  
PT particularly sterility.  
XX  
PS Claim 25; Page 42-43; 69pp; English.  
XX  
XX The present sequence encodes a floral homeotic protein, designated PTD.  
CC It is derived from Populus balsamifera subsp. trichocarpa. The  
CC specification also describes PTLF, PTAG-1 and PTAG-2 proteins. The floral  
CC homeotic proteins are expressed in floral tissues. PTLF is a homologue of  
CC LEAFY (LFY) and FLOXICANLA (FLO), and is expressed in immature  
CC inflorescences on which floral primordia are developing. PTD is a  
CC homologue of DEFICIENS (DEF), and is strongly expressed in stamens  
CC primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are  
CC homologues of AGAMOUS (AG). The floral homeotic proteins and  
CC polynucleotides are useful for producing transgenic plants having  
CC modified fertility characteristics, particularly sterility

XX SQ Sequence 681 BP; 228 A; 148 C; 157 G; 148 T; 0 U; 0 Other;  
Query Match 24.8%; Score 227.2; DB 4; Length 681;  
Best Local Similarity 58.4%; Pred. No. 3.3e-48;  
Matches 397; Conservative 0; Mismatches 283; Indels 0; Gaps 0;  
Qy 76 ATGGGAGAGGGGGAAGATAGATTAATAAAGATGAGAAATCCGACGAACAGGCAAGTTACA 135  
Db 1 ATGGGTCGTGGAAGATGAAATCAAGAAAGATGAAACCCCAACAGGCAAGTCACC 60  
Qy 136 TATTTAAGAGAGAGATGGATGATCTGAAGAGCCAGAGAGCTCATCTGTGTAT 195  
Db 61 TATTCGAAGAGAGAAATGATATTTCAAGAAAGCCCAAGAACTCACTGATCTTGTAT 120  
Qy 196 GCTCAGGTCCTCTCATCATGTTTCTCAAGCAAGAAAGTTGGCTGATTACTCAGCCCC 255  
Db 121 GCTAAGGTCCTCTTATCATGTTTCTCCAACTCACTAAGCAATCAATGATGATTAAGCCC 180  
Qy 256 TCTACTGATATTAAAGGGGATATATGAGAGGTACAGGTTGTGACTGGAATGATCTATGG 315  
Db 181 TCACATCGACAAAGAAAGATCTACATCAATATCAAGACCTTTAGCATAGATCTGTGG 240  
Qy 316 AATGCTCAGTATGAGAGATGAGAAATACGCTGAAGCATCTGAATGATTAACCAAAAC 375  
Db 241 GGCACTCAATACAGAAATGCAAGAGCACTTGAAGAGCTGATATCAATCATTAAG 300  
Qy 376 CTGAGAGAGAGATTGAGAGAGAGAGGAGGAGAAATTGAGGCAATGACATTAAGCAA 435  
Db 301 CTGAGACAAAGAAATCAAGGACAGAGAGAGAGGAGGAGGCTGAATGATCTGACATTAAT 360  
Qy 436 CTGGCGGCTTTAGAGAAATTTGGAAGACTCTCTTAAGATTGTTGGCATAGAAAGTAT 495  
Db 361 CTGGCGGCTTTAGAGCAATATGACTGAAGCCTTGAAATGTTGCTGGCAGAAAGTAC 420  
Qy 496 CATGTGATCGCCACACAACTGACACTTACAGAAAGGCTTAAGACACAAAGGAAACT 555  
Db 421 CATGTGATCAAAACACAAACGAAACCTTACAGAGAAAGGTGAAGATTTAGAGAGAGA 480  
Qy 556 TACCGGCTCTTAATACATGAACTGATATGAAAAGAGAGATCCGAATCGGTTTAAAT 615  
Db 481 CATGAAACCTCTTGAATGAAATGAAAGCAAAAACTAAGAGATGACAGTATGGTTAGTG 540  
Qy 616 GTAGAAAACCAAGTGAATTTATGAAAATTCGATTCCATGGATGATGATGATCCCTCAG 675  
Db 541 GACAAATGAAAGCTGCTGTGCACTTGCAAAATGGGGCTTCCAACTTATGCAATTCGCTG 600  
Qy 676 ATGTTTTCCTTGAAGGTTGTTCAATCCGATCAGCCCAATCGCTTGGTTAGGTTATGAA 735  
Db 601 CATCAGGGGACAAACCAACCAACATCTCTTAATCTTCACTTGAAGATGATTTGA 660  
Qy 736 TCACATGATCTTAGCCCTTGC 755  
Db 661 GCCCATGAACTTGCCCTTCC 680

RESULT 9  
AAZ57943 standard; cDNA; 924 BP.  
AAZ57943;  
AAZ57943;  
11-APR-2000 (first entry)  
DE Poplar floral homeotic gene PTD cDNA.  
XX  
XX Poplar; PTD; floral homeotic gene; transgenic plant; sterility;  
KM fertility; ss.  
XX  
XX Populus balsamifera subsp. trichocarpa.  
XX  
XX Key Location/Qualifiers  
FH 1. .684  
FT CDS

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FT      /*tag= a
FT      /note= "the coding region is also specifically claimed in
FT      Claim 1"
XX
XX      CA2227940-A1.
XX
XX      06-OCT-1999.
XX
XX      07-APR-1998; 98CA-02227940.
XX
XX      06-APR-1998; 98US-00080851.
XX
XX      (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX      Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;
XX
XX      MPI; 2000-106662/10.
XX
XX      P-PSDB; AAY58654.
XX
XX      Nucleic acid from Populus trichocarpa gene, useful for producing
XX      transgenic plants, particularly trees, with modified fertility
XX      characteristics such as sterility.
XX
XX      Claim 1; Page 46-47; 92pp; English.
XX
XX      The present sequence is that of cDNA encoding Populus balsamifera subsp.
XX      trichocarpa PTD protein (see AAY58654). The PTD gene (see AA257942) is 1
XX      of 4 newly identified floral homeotic genes from this poplar species. It
XX      is a homologue of DEFICIENTS and is expressed strongly in stamen primordia
XX      from the onset of organogenesis, and is also expressed at low levels in
XX      carpel primordia. The invention provides nucleic acid sequences of these
XX      4 Populus genes. The corresponding cDNA sequences (see AA257942-49) and
XX      deduced amino acid sequences (see AAY58454-57). It also provides methods
XX      of using the gene and cDNA sequences to produce genetically engineered
XX      Populus species and other trees having modified fertility
XX      characteristics, including sterility. Genetic constructs useful in
XX      producing genetically engineered Populus and other trees include
XX      antisense versions of PTD, dominant negative mutants, and constructs
XX      useful for sense suppression. Promoter sequences may be used to obtain
XX      floral specific expression of genes such as cyclooxins that may be used
XX      in genetic ablation strategies to produce trees having modified fertility
XX      characteristics, including sterility. Sterile trees allow increased wood
XX      yield and a reduction in the production of allergens such as pollen
XX
XX      Sequence 924 BP; 309 A; 185 C; 201 G; 229 T; 0 U; 0 Other;
SQ
Query Match      24.3%; Score 223.2; DB 3; Length 924;
Best Local Similarity 57.9%; Pred. No. 4e-47;
Matches 396; Conservative 0; Mismatches 288; Indels 0; Gaps 0;
QY      76 ATGGGAGGGGGAATGAGATGATTAAGATTAAGATTCGAGCAAGCAAGTATACA 135
DB      1 ATGGGTGTGGAAGATTGAATCAAGAGATCAAAACCCCAAAACAGCAAGTACC 60
QY      136 TATCTAAGAGAGAGTGGGATCTAGTAAAGGCCAAGAGACTCACTGTTCTCTGAT 195
DB      61 TACTCGAAGAGAGAAATGATTTTCAAGAAACCCCAAGAACTCATCTGATTTGAT 120
QY      196 GCTCAGGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGCTGATTAAGCAAGCCC 255
DB      121 GCTAAGGTCTCTTATCATATGTCCTCAACACTAACAACATCATGATTAAGCCCC 180
QY      256 TCTATCTGATTTAAGGGGATTAAGAGAGTACAGAGTGTGATCGAATGATCTATGG 315
DB      181 TCCACATCGAAGAAAGATCTAGATCAATATAGAAACGTTTAAAGCATAGATCTGG 240
QY      316 AATCTCAGTATGAGAGATGACAGATACGCTGAAGCATCTGATGATTAACCAAAAC 375
DB      241 GGCCTCATATCGAGAAATCAAGAGACTTGAAGAGCTGATGATTAATCAATCAAG 300
QY      376 CTGAGAGAGAGATTAAGAGAGAGAGAGGAGAGAAATTGAGGGCATGACATTAAGCA 435
DB      301 CTGAGAGAGAAATCAAGCAGAGAGAGAGAGAGGGCCCTGAATGATCTGAGCATTTGAT 360
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QY      436 CTGCGCGGCTTGTAGCAAACTTTGGAAGAGTCTTTAGATTGTTAGGCATAGAAAGTAT 495
DB      361 CTGCGCGGCTTGTAGCAAACTTTGGAAGAGTCTTTAGATTGTTAGGCATAGAAAGTAT 420
QY      496 CATGTGATGCGCAACACAACTGACATTAACAGAAAAGCTTTAAAGCAAGGAAACT 555
DB      421 CATGTGATCAAAAACAAAACGAAACCTTACAGAAAGAGTGAAGATTTAAGAGGAGA 480
QY      556 TACCGGCTCTAATATCATGACTGATATGAAGAGAGAGATCCGAACTAGCGTTTAAAT 615
DB      481 CATGAAACCTCTTGTAGAAATATGAGCAAACTAGAGAGATGACAGATATGTTAGTG 540
QY      616 GTAGAAAACCAAGATGAAATTTATGAAAATTCGATTCGAATGATAGTCTCTCAG 675
DB      541 GACAAAGAAAGCTGCTTGTGACATCTGCAATATGGGGCTTCCAACTCATCATCTCGCC 600
QY      676 ATGTTTCTTTAGGGTGTGATCCGAATCAAGCCCAATCTGCTGTTAGGTTATGAA 735
DB      601 CATCAGGAGACAAACACCAACCAATCTCCCTAATCTTCACTTGAGATGATTTGGA 660
QY      736 TCAATGATCTTAGCTTTCATPA 759
DB      661 GCCCATGAACCTTGCCTTCTTGA 684
RESULT 10
AAC5879
ID AAC5879 standard; DNA; 989 BP.
AAC5879;
25-JAN-2001 (first entry)
XX
DE Eucalyptus grandis transcription factor DNA sequence #10.
XX
XX plant; transcription factor; gene expression; eucalyptus; pine; acacia;
XX poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
XX basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
XX homeodomain zipper; LIM domain; AP2; ERBs; zinc finger domain;
XX type 2 Cys2His2; CCAAT box element; MYB; ss.
XX
XX Eucalyptus grandis.
XX
XX PN WC200053724-A2.
XX
XX PD 14-SEP-2000.
XX
XX PF 09-MAR-2000; 2000MO-US006112.
XX
XX PR 11-MAR-1999; 99US-00266513.
XX
XX PR 18-AUG-1999; 99US-0149485P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX (FLEET-) FLETCHER CHALLENGE FORESTS LTD.
XX
XX PI Wood M, McGrath A, Shenk MA, Glenn M;
XX
XX MPI; 2000-579369/54.
XX
XX New isolated polynucleotide encoding a plant transcription factor for
XX producing a plant e.g. a woody plant, preferably eucalyptus or pine,
XX having modified gene expression or modified activity of a polypeptide.
XX
XX Claim 1; Page 46-47; 747pp; English.
XX
XX The present invention relates to novel plant transcription factors from
XX Eucalyptus grandis or Pinus radiata. The present sequence is the coding
XX sequence for one such transcription factor. The transcription factor may
XX be used to produce a plant having modified gene expression such as a
XX woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
XX mahogany species or to modify the activity of a polypeptide in a plant.
XX The transcription factors of the present invention are members from the
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PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
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PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147182P.
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PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160981P.
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PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
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PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.

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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

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Query Match      23.4%; Score 214.4; DB 3; Length 954;
Best Local Similarity 61.4%; Pred. No. 7.4e-45;
Matches 344; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

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QY 49 AACAGGAGGAGAACAGGAGAGAGAGATGGGAGGGGAGATAGATATAAAAAAGTA 108
DB 2 AAAAAAGTTAAACAAAGAGAGAGATATGGCGAGAGGAGAGATCCAGAGAGATA 61
QY 109 GAGATCCGACGACGACGCAAGTTACATATTTCTTAAGAGAGAGTTGGATCTGAGAG 168
DB 62 GAGAACGACGACAAACGACAGAGATGAGTATTCAAAGAGAAAGATGTTATTCAGAAA 121
QY 169 GCCAAGAGCTCATCTGTTCTGTGATGCTCAGGTCTCTCATCATGTTCTCAAGACA 228
DB 122 GCAATGAGCTCAGCGTTTGTGTGATGCTAGGGTTTCATTTATCATGTTCTTAGTCC 181
QY 229 GGAAGTTGGCTGATTACTGCAACCCCTCTACTGATATTAAAGGAGATATAGAGTAC 288
DB 182 AACAGCTTATAGATATATACGCCCTAACACCAACAGAGAGATCTGATCTGTAC 241
QY 289 CAGGTTGTGACTGGAATGATCTATGGAATGCTCAGTATAGAGAGATGCAATACGCTG 348
DB 242 CAAACTATTTCTGATGTCGATGTTTGGCCACTCAATATAGCGAATGCAAGAAACAG 301
QY 349 AAGATCTGAATGATTAACAAACCTGAGAGAGAGATTAGAGAGAGAGAGAGAG 408
DB 302 AGAAACTGTTGAGACAAATAGAAATCTCCGATCAGATCAAGCAGAGGCTAGGTAG 361
QY 409 GAAATGAGGCGATGACATTAAGCAACTGCGCGGTCTTGAGCAAACTTGGAGAGCT 468
DB 362 TGTTTGACGAGCTGACATTCAGAGAGCTCGTGTGTTGAGTGAATGAAAAACAT 421
QY 469 CTTGAATTTGTAGGCAATAGAAATATCATGTATGCGCCACAAACTGACCTTAAG 528
DB 422 TTCAACTCGTTCGCGAGCCCAAGTTCAAATCTCTTGGGATCGAATCGAGACACAG 481
QY 529 AAAAAGCTTAAGCAACAGGAACTTACCGGCTTAATATCATGATGATGATGAAA 588
DB 482 AAAAAGCAAAAGTCAACAAGACATACAAAGAAATCTCATACATGAGCTGGAATAGA 541
QY 589 GAGGAGATCCGAACTACGG 608
DB 542 GCTGAGATCTCTCATATGG 561

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RESULT 13
AAC51790
ID AAC51790 standard; DNA; 1170 BP.
XX AAC51790;
AC AAC51790;
XX 18-OCT-2000 (first entry)
DT 18-OCT-2000
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 69758.
DE Arabidopsis thaliana
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX EPI033405-A2.
XX EPI033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX PF
XX
XX

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PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

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Query Match 23.3%; Score 213.8; DB 3; Length 1170;

Best Local Similarity 60.3%; Pred. No. 1,1e-44;

Matches 353; Conservative 0; Mismatches 232; Indels 0; Gaps 0;

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QY 24 AAGAGAGGGTGTGAACAGAGGAAACAGGGGAGAAACAGAGAGAGATGGGAG 83
DB 201 AAGAGAGGGTGTGAACAGAGGAAACAGGGGAGAAACAGAGAGATGGGAG 260
QY 84 GGGAGAGTATGAGATTAAGAAAGATGAGATCCAGAGAGAGAGATTAATTTCA 143
DB 261 AGGAGAGTATGAGATTAAGAAAGATGAGATCCAGAGAGAGAGATTAATTTCA 320
QY 144 GAGAGAGTGGGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 203
DB 321 GAGAGAGAGTGGGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 380
QY 204 CTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 263
DB 381 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 440
QY 264 TATTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 323
DB 441 AAGAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 500
QY 324 GTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 383
DB 501 ATATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 560
QY 384 GAGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443
DB 561 TCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 620
QY 444 TCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 503
DB 621 TCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680
QY 504 GCGCACACAACTGACCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563

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DB 681 TGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740
QY 564 TCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608
DB 741 TCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 785

RESULT 14
ADO61550
ADO61550 standard; DNA; 988 BP.
XX
XX ADO61550;
AC
XX 15-JUL-2004 (first entry)
DT
XX Transcription factor G133 coding sequence, SEQ ID 17.
DE
XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;
KW osmotic stress tolerance; cold tolerance; heat tolerance;
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
KW glyphosate resistance; flowering; fertility; seed development; ds.
OS
XX Arabidopsis thaliana.
OS
XX W02004031349-A2.
PN
XX 15-APR-2004.
PD
XX 18-SEP-2003; 2003WO-US030292.
PF
XX 18-SEP-2002; 2002US-0411837P.
PR 17-DEC-2002; 2002US-0434166P.
PR 24-APR-2003; 2003US-0465809P.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
XX Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;
PI Rieckmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK;
XX
XX WPI; 2004-330163/30.
DR
XX P-PSDB; ADO61551.
PT
XX New recombinant polynucleotide encoding transcription factor
PT polypeptides, useful for producing transgenic plants with advantageous
PS properties compared to a reference plant.
XX
XX Claim 1; SEQ ID NO 17; 510bp; English.
XX
XX The present invention relates to novel plant transcription factor
XX proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
XX sequences can be used to produce transgenic plants, which overexpress
XX (II), where the transgenic plant has an altered trait as compared to a
XX non-transgenic plant or wild-type plant. The transgenic plant comprises
XX an altered trait selected from increased tolerance to abiotic stress,
XX increased tolerance to osmotic stress, increased tolerance to cold,
XX increased germination in cold, increased tolerance to heat, increased
XX germination in heat, increased tolerance to freezing conditions,
XX increased tolerance to low nitrogen conditions, increased tolerance to
XX low phosphate conditions, increased tolerance to disease, including
XX fungal disease and particularly Erysiphe, Fusarium and Botrytis,
XX increased tolerance to multiple fungal pathogens, increased resistance to
XX glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
XX increased sensitivity to ACC, altered sugar sensing, increased tolerance
XX to sugars, altered carbon/nitrogen sensing, early flowering, late
XX flowering, altered flower structure, loss of flower determinacy, reduced
XX fertility, altered shoot meristem development, altered branching pattern,
XX altered stem morphology, altered vascular tissue structure, reduced
XX apical dominance, altered trichome density, altered trichome development,
XX altered trichome structure, altered root development, altered shade
XX avoidance, altered seed development, altered seed ripening, altered seed
XX germination, slow growth, fast growth, altered cell differentiation,
XX altered cell proliferation, altered cell expansion, altered phase change,
XX altered senescence, abnormal embryo development, altered programmed cell

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CC death, lethality when overexpressed, altered necrosis patterns, increased  
CC plant size, increased biomass, large seedling, dwarfed plants, dark  
CC green leaves, change in leaf shape, increased leaf size and mass, light  
CC green or grey leaves, glossy leaves, altered abaxial/adaxial polarity,  
CC altered seed coloration, altered seed size, altered seed shape, large  
CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil  
CC content, altered seed protein content, altered seedprenyl content,  
CC altered leaf prenyl lipid content, increased anthocyanin levels, and  
CC decreased anthocyanin levels. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 988 BP: 326 A; 194 C; 202 G; 266 T; 0 U; 0 Other;

Query Match 23.28; Score 213.2; DB 12; Length 988;

Best Local Similarly 61.28; Pred. No. 1.5e-44;

Matches 344; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

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DT 17-OCT-2000 (first entry)  
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KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.

XX Arabidopsis thaliana.  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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7: gb\_est6.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SOURCE Liriodendron tulipifera  
ORGANISM Liriodendron tulipifera  
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dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,  
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Lebens-Mack, J., Landherr, L., Schlarbaum, S., Ilut, D. and Wall, K.  
Generation of ESTs from early flower buds of Liriodendron  
tulipifera  
Unpublished (2003)  
Contact: Claude dePamphilis or James Lebens-Mack  
Mueller Laboratory  
Penn State University  
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn  
State University, University Park, PA 16802, USA  
Tel: 814 863 6413  
Fax: 814 865 9131  
Email: cwd3@psu.edu or jh110@psu.edu  
The sequence provided is trimmed of vector and low quality regions.  
Full sequence and original trace file are available from the Plant  
Genome Network website (http://pgn.cornell.edu)  
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the Floral Genome Project (FGP). The Floral Genome Project

## ORIGIN

is funded by NSF's Plant Genome Research Program  
(DBI-0115684). More information about the project can be  
obtained at <http://fgrp.bio.psu.edu>

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Query Match      30.8%; Score 282.4; DB 7; Length 615;
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DB 306 AGGCAAGAGCTTATGGAATCTCTACAGAGAAATGCAAGATCACTTGAACAACTCA 365
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QY 360 TGAATTAACCAAAACCTGAGAGAGAGATTAAGAGAGAGAGAGAGAGATTTGAGAG 419
    |||
DB 366 AGAGATTAATTAACAGTCTCCGAGAGGCAATCAGGCATAGATCGGTGAATCTGAGCA 425
    |||
QY 420 CATGACATTAAGCACTGCGCGGTCTTGAGCAAACTTTGAAAGAGTCTTGAATTTG 479
    |||
DB 426 TCTGGAATTAAGAAACTGCGCGGTCTTGAGCAAACTTTGAAAGAGTCTTGAATTTG 485
    |||
QY 480 TAGGATTAAGAAATGATCATGATCGGCACAACTGACACTTACAAAGAAAGCTTAA 539
    |||
DB 486 TCCGAAAGAGATATCATGTGATCAACTCAACAGAGAGACTTACAAAGAAAGTTGAG 545
    |||
QY 540 AAGCACAAGGAAACTTACCGCGCTCTAATATCATGAATCTGATTA 583
    |||
DB 546 AATCTGACAGAGACAGCAATTTTATTCGGAAATTTGGGTA 589
    |||

RESULT 2
CB626851 585 bp mRNA linear EST 08-APR-2003
LOCUS OS1IB01G03.f OS1IB Oryza sativa (indica cultivar-group) cDNA
DEFINITION clone OS1IB01G03 5', mRNA sequence.
ACCESSION CB626851 GI:29621840
VERSION CB626851.1
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriharitoidae; Oryzaceae; Oryza.
1 (bases 1 to 585)
Jantseurirarat.C., Lu.G., Gowda.M., Hatfield.J., Zhou.B., Mazur.B.,
Kudrna.D., Dean.R., Soderlund.C., Wing.R. and Wang.G.
large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

```

## FEATURES

PCR primers  
FORWARD: gta aac cga cgg cca gtc  
BACKWARD: gga aac agc tat gac cat g  
Plate: 01 row: G column: 03  
Seq primer: gta aac cga cgg cca gtc.  
Location/Qualifiers  
1..585  
/organism="Oryza sativa (indica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="IR36"  
/db\_xref="taxon:39946"  
/clone="OS1IB01G03"  
/issue\_type="Leaf"  
/dev\_stage="3 week"  
/lab\_host="DH10B"  
/clone\_1lb="OS1IB"  
/note="Vector: pBluescript II KS +, Site\_1: EcoRI, Site\_2:  
XhoI, 24 hrs after inoculation with Rice Blast (P06-6-3)"

## ORIGIN

```

Query Match      28.5%; Score 261.6; DB 6; Length 585;
Best Local Similarity 68.2%; Pred. No. 8.1e-52;
Matches 363; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGAGAGATAGAGATTAATAAAGATAGAGATCCGACGAACGAGCAAGTTACA 135
    |||
DB 30 ATGGGAGGGGAGAGATAGAGATTAATAAAGATAGAGATCCGACGAACGAGCAAGTTACA 89
    |||
QY 136 TATTTAAGAGAGAGATTGGGATCTGAAGAGGCCAAGAGCTCTCTTCTGTGAT 195
    |||
DB 90 TACTCGAAGCGCGCAACGGGATCATAGAAAGGCCAGGAGACTCAAGTCTCTGCGAC 149
    |||
QY 196 GCTCAGGCTCTCTCATCATGTTCTCAAGCACAGGAAAGTTGGCTGATTAATGACAGCCCC 255
    |||
DB 150 GCCAGAGTCCCATCATCATGTTCTCTCAAGCACAGGAAAGTTGGCTGATTAATGACAGCCCC 209
    |||
QY 256 TCTACTGATTAAGAGGATATATAGAGATCAAGTTGATCTGAATGATCTTATG 315
    |||
DB 210 TCCACCGAATCAAGGAGATCTTGAACCGCTACAGCAAGCATCGGACAGCTTTGG 269
    |||
QY 316 AATGCTCATTAAGAGAGATGCAAGATACGCTGAAGCATCTGAATGATTAACCAAAAC 375
    |||
DB 270 ATCGAGCAGTATGAGATATGACAGCGACGCTGAGCATCTCAAGGACATCAACCGCAAC 329
    |||
QY 376 CTGAGAGAGAGATTGAGAGAGAGAGAGGAGAGAAATTTGAGAGGACATGAATTAAGCA 435
    |||
DB 330 CTGCGCACGAGATCAAGCAAGAGATGAGAGAGATCTGAGAGGCTGAGATTCAGCAG 389
    |||
QY 436 CTGCGCGGCTTGAAGCAAACTTTGAGAGAGTCTTGAATTTGATAGGATTAAGAAATAT 495
    |||
DB 390 CTGCGCGGCTTGAAGCAAAATGTCATGTCGCCCTCAAGAGAGTTGCGCACAGAGATAT 449
    |||
QY 496 CATGTGATGCGCACACAACTGACACTTCAAGAGAAAGCTTAAAGACCAAGGAAACT 555
    |||
DB 450 CATGTGATGCGCACACAGACTGAACCTTCAAGAGAAAGCTTAAAGACCTTCAAGGAGG 509
    |||
QY 556 TACCGGCTCTAATATACATGATGATGAAGAGAGAAATCCGAACACG 607
    |||
DB 510 TACAAGACTCTGACAGAGAGCTGGGCTTGTGCGAGAGCCGCGCTGCTTCG 561
    |||

RESULT 3
CB971393 762 bp mRNA linear EST 30-APR-2003
LOCUS CAB10005_11a_Fa_B07 Cabernet Sauvignon flower Pre-bloom - CAB1
DEFINITION Vitis vinifera cDNA clone CAB10005_11a_Fa_B07 5', mRNA sequence.
ACCESSION CB971393
VERSION CB971393.1 GI:30254946
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

rosids; Vitaceae; Vitis.  
1 (bases 1 to 762)  
Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leele, A., Xu, J.,  
Jones, K. and Cook, D.  
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'  
berries at various developmental stages  
Unpublished (2003)  
Contact: Douglas Cook, PhD  
CAES Genome Facility  
UC Davis, Plant Pathology  
One Shields Ave, Davis, CA 95616, USA  
Tel: 530 754 6561  
Fax: 530 754 6617  
Email: drcoc@ucdavis.edu  
Seq primer: ACGGTACCGACATATGCC.  
Location/Qualifiers

FEATURES  
source

1..762  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="CAB10005\_Ia\_Pa\_B07"  
/sex="Hermaphrodite"  
/dev\_stage="Pre-bloom"  
/lab\_host="DHSalpha"  
/clone\_id="Cabernet Sauvignon Flower Pre-bloom - CAB1"  
/note="Organ: Flower - Pre-bloom; Vector: pDNR; Site\_1:  
SflI; Site\_2: SflI; CAB1 is a cDNA library of Vitis  
vinifera cv. 'Cabernet Sauvignon' clone 8 flowers. Samples  
were collected approximately eleven days before onset of  
bloom (clusters at this stage were fully developed and  
flowers with calypters or caps still attached. Sampled  
vines were located at the University of California, Davis,  
Experimental Vineyard. cDNAs were made by oligo-dT priming  
and directionally cloned. 5' and 3' adaptors were used in  
cloning as follows:  
5'-AAGCAGGTGATCAACGAGAGTGCCATTACGCCGGG-3' and  
5'-ATTCTAGAGCGGCGCGCCAGCATG-DT(30)NN-3'. Library was  
constructed using the Clontech Creator SMART kit and  
size-selected to contain the 0.5-3 kb size fraction."

## ORIGIN

Query Match 28.1%; Score 257.8; DB 6; Length 762;  
Best Local Similarity 67.3%; Pred. No. 6.9e-51;  
Matches 364; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

68 AGAAGAGATGGGAGGGGGAATAGATTAATAATGAGATCCGAGCAAGC 127  
2 AGGAGGTATGCTAGAGAAAGATTGATCAAGAGATAGAACTGACGACAGGC 61  
128 AAGTTACATTTCTAAGAGAGATTGGGATCTGAAAGAGCCAGAGCTCACTTTC 187  
62 AGGTCACTTCTCAAGAGAGAAATGATCTTCAAGAGCCAGTGAAGCTCACTGTTTC 121  
188 TCTGTGATGCTCAAGGTCTCTCTCATCATGTTCTCAAGCAAGAAAGTTGGCTTACT 247  
122 TTGTGATGCTAAGGTTTCTATCATCATGCTCTCCAGTACGAAAGCTCCATGAATACA 181  
248 GCAAGCCCTTACTGATATTAAGGGGATATAGAGATACAGGTTGTGACTGGAATGG 307  
182 TCAGCCCTTCCATCAAGAAAGAAATATTGATCACTGACCAAGCACTCTAGAGATGG 241  
308 ATCTATGAGATGCTCATGATAGAGATGACAGATACCTGAGCATCTGATGATTA 367  
242 ATCTATGAGATGCTCATGATAGAGATGACAGATACCTGAGCATCTGATGATTA 301  
368 ACCAAACCTGAGAGAGATTAAGAGAGAGAGAGAGAGAGATTAAGAGGCGATGACA 427  
302 ACAAGATCTCAGAGAGAGATTAAGAGAGAGATGAGAGATTAAGAGGCGATGACA 361  
428 TTAAGCAATGCGCGCTTTGAGCAAACTTTGAGAGAGCTCTTGAATGTTTGAAGCATA 487  
362 TTGAGAACTGCGAGATCTTGAACAAAGATGAGAGAGATTTTGAAGATGGTTCGTGATA 421

QY 488 GAAGTATCATGTGATCGCCACACAACTGACACTTACAAAGAAAGCTTAAGACAA 547  
DB 422 GGAAGTACCAAGGATCAATATCATGATTAAGAACTTTCAAGAAAGAGTAAAGAAATGG 481  
QY 548 GGAAGTACCAAGGATCAATATCATGATTAAGAAAGTAAAGAGAAATCCAGACTAG 607  
DB 482 AACAATACCAAAATCTCTCATGATTTGATGACAGGAGCAGAGATCATATCATG 541  
QY 608 G 608  
DB 542 G 542

RESULT 4  
CB972246 692 bp mRNA linear EST 30-APR-2003  
LOCUS CB972246  
DEFINITION CAB10006\_Ia\_Pa\_D07 Cabernet Sauvignon Flower Pre-bloom - CAB1 Vitis  
vinifera cDNA clone CAB10006\_Ia\_Pa\_D07 5', mRNA sequence.  
ACCESSION CB972246  
VERSION CB972246.1 GI:30256403  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Vitis vinifera  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 692)  
Jones, K. and Cook, D.  
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'  
berries at various developmental stages  
Unpublished (2003)  
Contact: Douglas Cook, PhD  
CAES Genome Facility  
UC Davis, Plant Pathology  
One Shields Ave, Davis, CA 95616, USA  
Tel: 530 754 6561  
Fax: 530 754 6617  
Email: drcoc@ucdavis.edu  
Seq primer: ACGGTACCGACATATGCC.  
Location/Qualifiers

FEATURES  
source

1..692  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="CAB10006\_Ia\_Pa\_D07"  
/sex="Hermaphrodite"  
/dev\_stage="Pre-bloom"  
/lab\_host="DHSalpha"  
/clone\_id="Cabernet Sauvignon Flower Pre-bloom - CAB1"  
/note="Organ: Flower - Pre-bloom; Vector: pDNR; Site\_1:  
SflI; Site\_2: SflI; CAB1 is a cDNA library of Vitis  
vinifera cv. 'Cabernet Sauvignon' clone 8 flowers. Samples  
were collected approximately eleven days before onset of  
bloom (clusters at this stage were fully developed and  
flowers with calypters or caps still attached. Sampled  
vines were located at the University of California, Davis,  
Experimental Vineyard. cDNAs were made by oligo-dT priming  
and directionally cloned. 5' and 3' adaptors were used in  
cloning as follows:  
5'-AAGCAGGTGATCAACGAGAGTGCCATTACGCCGGG-3' and  
5'-ATTCTAGAGCGGCGCGCCAGCATG-DT(30)NN-3'. Library was  
constructed using the Clontech Creator SMART kit and  
size-selected to contain the 0.5-3 kb size fraction."

## ORIGIN

Query Match 27.8%; Score 255.2; DB 6; Length 692;  
Best Local Similarity 65.4%; Pred. No. 2.9e-50;  
Matches 374; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

QY 37 AGAACAGAGAAACAGGCGAGAAACAGGCGAGAGAGAGATGGGAGGCGGAATAGAG 96

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Db      12 AGAAGGATCTGGAATCGAGGAGAGAGAGAGATGCTAGAGAAAGATTGAG 71
Qy      97 ATAAAAAAGATAGAGATCCGACGAAACAGGCAAGTTACATATTCTAAGAGAGATTGGG 156
Db      72 ATCAAAAGATAGAGACTCGACGAAACAGGCAAGTCACTACCAAGAGACGAAATGGT 131
Qy      157 ATACGAAAGAGGCGAAGAGCTCAGTGTCTCTGTGATGCTCAGAGCTCTCATCATG 216
Db      132 ATCTCAAGAGGCGAGTGAATCACTGTTCTTTGTGATGCTAAGTTCTATCATCATG 191
Qy      217 TTCTCAAGCAAGAAAGTTGCTGATTAATGACGCCCTCTAATGATTTAAGGGAGTA 276
Db      192 CTCTCAGATCTGGAAGAGCTCCATGAATACATGAGCCCTTCCACTCAACGAAACAAATA 251
Qy      277 TATGAGAGTACCAAGTTGTGACTGAGATGATCTAATGAACTCTCATATGAGAGATG 336
Db      252 TTTGATCAGTACCAAGACACTTGAAGGTGATCTATGAGCTATCATATGAGAGAAATG 311
Qy      337 CAGAATACGCTGAAGATCTGAATGATTAACCAAAACCTGAGGAAGAGATTAGAGAG 396
Db      312 CAGAAAGAACTTGAGAAAGCTGAAAGATGTGAACAAGATTCAGAAAGAGATTAGGACG 371
Qy      397 AGGAAGGGAGGAAATTTGAGGCAATGACATAAAGCAACTGCGCGTCTTGAAGCAACT 456
Db      372 AGGATGGGTGAACATTTGAGCGATTTGAGCGTTGAGGAATCGGAGATCTTGAACAAG 431
Qy      457 TTGGAAGAGTCTCTTGAATTTGTTAGCATAGAAAGTATCATGTGATCGCAACAAC 516
Db      432 ATGCAAGATCTTTGAAGATGTTGTTGATGATGAGATCCAGGTGATCAATATCAGATT 491
Qy      517 GACACTTACAAAGAAAGCTTAAGAGCAAGAGGAAACTTACCGCGCTTAATACATGAA 576
Db      492 GAAACTTTCAAGAAAGCGTTAAGATGTGGAACAAATATCAAAAATCTCTACATGAA 551
Qy      577 CTGATATGAAAGAGAGAAATCCGAATACG 608
Db      552 TTTGATGCAAGGACAGAGATCAATCTATG 583

RESULT 5
CB921382 694 bp mRNA linear EST 25-APR-2003
LOCUS VVD070D08 353397 An expressed sequence tag database for abiotic
DEFINITION stressed Berries of Vitis vinifera var. Chardonnay Vitis vinifera
CDNA clone VVD070D08 5, mRNA sequence.
CB921382
VERSION CB921382.1 GI:30136044
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Bukharjota; Vitridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 694)
Cushman,J.C.
An expressed sequence tag database for abiotic stressed berries of
Vitis vinifera var. Chardonnay
Unpublished (2002)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRIMERs
FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 070 row: D column: 08
Seq primer: T3 20mer
High quality sequence stop: 694.
FEATURES
Location/Qualifiers
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source
1..694
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVD070D08"
/tissue_type="berries"
/dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/clone_1lb="An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay"
/note="Vector: lambda Uni-zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

ORIGIN
Query Match 27.4%; Score 250.8; DB 6; Length 694;
Best local similarity 61.3%; Pred. No. 3.3e-49;
Matches 424; Conservative 0; Mismatches 262; Indels 6; Gaps 1;

Qy      79 GGAAGGGGAGATAGATATAAAGATAGAAATCCGACGACAGCAAGCAATTAAT 138
Db      1 GGTCTGGGAAATTTGAGATCAAGAGATAGAGAAACCCACCAAGAGCGATCACTAC 60
Qy      139 TCTAAGAGAGATTGGGATCTGAAGAGCGCAAGAGCTCACTGTTCTGTGATGCT 198
Db      61 TCCAAAGCAGAAATGTAATTTTCAAGAAAGCCAGAGCTCACGTTCTTGTGATGCT 120
Qy      199 CAGGTCTCTCATCATGTTCTCAAGCACAGGAAAGTTGGCTGATTAATCTGAGCCCTCT 258
Db      121 AAGTTTCACTCATCATGTTCTTCCAAATCTGAAATTTCCAGAAATATACAGTCTACT 180
Qy      259 ACTGATATTAAAGGGATATATAGAGGTACCAAGTTGTGATCTGAAATGATCTTAAGAT 318
Db      181 ATACACAGAAAGAGGTCTACATCATCATGATCAAGAACTTTGAGGATGATCTTTGGAC 240
Qy      319 GCTCGATAGAGAGATGAGAAATACGCTGAAGCATCTGAATGAGATTAAACAAACCTG 378
Db      241 TTTCACTACAGAGAAATGCAAGAAACTTGCAGAAATCTGAAGAGTCAACAACAATTA 300
Qy      379 AGGAAGAGATTAGAGAGAGAGGAGAGATTGAGGAGCATGACATAAGCAACTG 438
Db      301 AGGAGAGATCAAGGAAAGAAATGGGTGAAGTTGGGGGATCTGACATTGAGGACCTG 360
Qy      439 CGCGTCTTGAAGAACTTTGAGAGAGTCTTGAATTTGATGAGCATAGAAATGATCAT 498
Db      361 CGGGGCTTGAAGAGAGATGAGACGCTTCTTGAATTTGATGAGCGGACGAGAACTGAC 420
Qy      499 GTGATGCCACCAACCTACCTTACAGAAAGAGCTTAAGAGCAAGAGAACTTAC 558
Db      421 GTGATCAAAACTGAGCCGAGACCTACAGAAAGAGTCAAGAACTTGAAGACACAC 480
Qy      559 CGGCTCTAATCATGAATCTGATATGAAGAGAGAAATCCGAATACCGTTTAAATGTA 618
Db      481 GGAATCTCTCTCTCAACTTTGAGGCAAAATGAGATGCCATTAAGGAT-----TA 534
Qy      619 GAAACCAAGTAGAATTTATGAAATTTGATTCATGATGTAAGAGTGTCTCAGATG 678
Db      535 GTGAAAGAAAGATGAGATATGATATCAGCGGTGCAATTTGCAAGCGGCTTCAACCTC 594
Qy      679 TTTTCTTTAAGGTTGTTGATCGAATCAGCCCAATCTGCTGTTAGTATGAATCA 738
Db      595 TATGCTTTTCGCTGTGATGAGGCCCTTAATCTTACACATGATGGGGATATGATCA 654
Qy      739 CATGATCTTAGCCTTGCAATATGAGCAATTAAT 770
Db      655 CATGATCTGCGCTTCTGATCATAGTACAT 686

RESULT 6
BU994760 651 bp mRNA linear EST 23-OCT-2002
LOCUS HM08C02 HM Hordeum vulgare subsp. vulgare CDNA clone HM08C02
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BU994760
VERSION BU994760.1 GI:24271743
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KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Bukarjoca; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
1 (bases 1 to 651)  
REFERENCE Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.  
AUTHORS EST sequencing and analysis in barley (2002)  
JOURNAL Unpublished (2002)  
COMMENT Contact: Stein Nils  
Molecular Markers Group, Department Genbank  
Institute of Plant Genetics and Crop Plant Research (IPK)  
Corrensstr. 3, 06466, Gatersleben, Germany  
Tel: 039482-5522  
Fax: 039482-5595  
Email: stein@ipk-gatersleben.de  
Insert length: 651 Std Error: 0.00  
Plate: 8 row: C column: 2  
Seq primer: M13rev.  
Location/Qualifiers  
1. 651  
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/cultivar="barke"  
/sub\_species="vulgare"  
/db\_xref="GABI:254578"  
/db\_xref="taxon:112509"  
/clone="HM08C02"  
/tissue\_type="male inflorescences"  
/dev\_stage="male inflorescences (approx. 2 mm in size),  
green anther stage"  
/lab\_host="XL10-Gold"  
/clone\_lib="HM"  
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of  
cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning  
artefact caused by the kit, in most cases the EcoRI site  
is NOT present, as well as the EcoRI adapter used for  
cloning. To excise the insert, restriction sites upstream  
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also  
due to the cloning system used Blue/white selection for  
recombinants is not 100% reliable."

ORIGIN  
Query Match 26.8%; Score 246; DB 5; Length 651;  
Best Local Similarity 69.1%; Pred. No. 4.5e-48;  
Matches 336; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 73 GAGATGGGGAGGGGGAAGATGAGATTAATAAAGATGAGAAATCCGACGACGACGAGTT 132  
DB 150 GAGATGGGGGCGGGGGAAGATCGAGATTAAGCGATCGAAGCCGACGACGACGAGTTG 209  
QY 133 ACATATTTTAAGAGAGAGTTGGATCTACTGAAGAGCGCAAGAGCTTCTCTGT 192  
DB 210 ACCTATCTCAAGCGCGGTCCGGATTCATGAAGAGGGCGGAGCTTACCGTGTCTGC 269  
QY 193 GATGCTGAGTCTCTCTCATGATGTTCTCAAGCACAGGAAGTTGGCTGATTACTGCAGC 252  
DB 270 GAGCGCCAGGTGCGCATCATCTGTTCTCTCCACCGGCAAGTACCAAGATTTGCGAGC 329  
QY 253 CCCTTACTGATATTTAAGGGGATATATGAGAGGTAACAAGTTTGACTGGAATGAGATT 312  
DB 330 ACCGACCGACATCAAGGGGATCTTTGACCGGTACGACGAGGCGCATCGGACCGAGCTG 389  
QY 313 TGGATGTCTAGTATGAGAGATGAGAAATCGCTGAGCAATCTGAATGAGATTAAACAA 372  
DB 390 TGGATCGAGCATATGAGAAATATGAGCGACGCTGACCGCATCTCAAGACATCAACAGG 449  
QY 373 AACCTGAGGAAGAGATTAGAGAGAGAGGGGAGGAATTGAGGGGATGAGCACTAAAG 432  
DB 450 AACCTGCGCACCGAGATCAAGGCAAAAGATGGTGAAGATCTGAGACGCGCTGAGATTGAG 509  
QY 433 CAACCTGCGCGGCTTTGAGCAAACTTTGAGAGAGTCTTTAGAAATTTTGAAGCATGAAAG 492

DB 510 GAGCTCGGGGCGCTTAGCAAAATGTCGATGCGGCTCTCAAGAGAGTTGCCAGAGGAAG 569  
QY 493 TATCATGTATGCCACACAACTGACACTTTCAGAAAAAGCTTTAAAGCACAGGAA 552  
DB 570 TATCATGTATACACACAGACTGAACCTTCAAGAAAGAGTGAAGCATCTCCAGAG 629  
QY 553 ACTTAC 558  
DB 630 GCATAC 635

RESULT 7  
CO995351 591 bp mRNA linear EST 18-AUG-2004  
LOCUS eca01-5c81-g10 5', mRNA sequence.  
DEFINITION eca01-5c81-g10 5', mRNA sequence.  
ACCESSION CO995351  
VERSION CO995351.1 GI:51354575  
KEYWORDS EST.  
SOURCE Eschscholzia californica (California poppy)  
ORGANISM Eschscholzia californica  
Bukarjoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;  
Papaveraceae; Eschscholziaceae; Eschscholzia.  
1 (bases 1 to 591)  
REFERENCE depamphilis, C., Carlson, J., Ma, H., Tanksley, S., Field, D.,  
AUTHORS leebens-Mack, J., Arrington, J., Zahn, L.M., Kong, H., Ilut, D.,  
Druckemiller, M., Landherr, L., Hu, Y., Plock, S., Wall, K.,  
Chioresan, S., Albert, V., Doyle, J., Frolich, M., Miller, W.,  
Oppenheimer, D., Solits, D., Solits, P. and Theissen, G.  
Generation of ESTs from early flower buds of Eschscholzia  
californica  
TITLE Unpublished (2002)  
JOURNAL Contact: Claude depamphilis or James leebens-Mack  
COMMENT Mueller Laboratory  
Penn State University  
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn  
State University, University Park, PA 16802, USA  
Tel: 814 863 6413  
Fax: 814 865 9131  
Email: cwid@psu.edu or jh110@psu.edu  
The sequence provided is trimmed of vector and low quality regions.  
Full sequence and original trace file are available from the Plant  
Genome Network website (<http://psn.cornell.edu>)  
Plate: eca01-5c81 row: 9 column: 10  
Seq primer: M13P.  
Location/Qualifiers  
1. 591  
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/db\_xref="taxon:3467"  
/clone="eca01-5c81-g10"  
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/dev\_stage="millimeter buds"  
/lab\_host="SOLR"  
/clone\_lib="eca01"  
/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;  
Site 2: XhoI; Plants were grown in greenhouse at Penn  
State from commercially available seeds. Only floral buds  
with diameter of 2.5 mm of less were collected. This is a  
directionally cloned, non-normalized library. Avg. insert  
length: 1702; Primers: M13P and M13R; Antibiotic: 50 ug/ml  
Ampicillin; Primary Titer: 786 pfu total; Amplified Titer:  
1.68B1 pfu/ml; Mass Excised Titer: 5.658 total; This  
library has been generated by the Floral Genome Project  
(FGP). We would like to thank Huck life Sciences  
Consortium for their assistance. The Floral Genome Project  
is funded by NSF's Plant Genome Research Program  
(DBI-0115684). More information about the project can be  
obtained at <http://fgp.bio.psu.edu>

ORIGIN



BE497689 645 bp mRNA linear EST 04-AUG-2000  
 LOCUS BE497689  
 DEFINITION WHE955\_D02\_G03S Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE955\_D02\_G03, mRNA sequence.  
 ACCESSION BE497689  
 VERSION BE497689.1 GI:9696306  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.  
 REFERENCE 1 (bases 1 to 645)  
 Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Heia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.  
 The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library  
 Unpublished (2000)  
 JOURNAL Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105595773  
 Fax: 5105595818  
 Email: oanderson@pw.usda.gov  
 Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20  
 Seq primer: Stragene SK primer.  
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 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="Chinese Spring"  
 /db\_xref="taxon:4565"  
 /clone="WHE955\_D02\_G03"  
 /issue\_type="Spike before anthesis"  
 /dev\_stage="Adult plant"  
 /lab\_host="E. coli SOLR"  
 /clone\_lib="Wheat pre-anthesis spike cDNA library"  
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site\_1: EcoRI; Site\_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagemids in the T7 Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

Db 345 TGGATCGACGATATAGATATATGACGCCACGCTGAGCATTCAGAGACATCAATCCG 404  
 Qy 373 AACCTGAGGAAGAGATTGAGAGAGAAAGGGAGAAATTGGAGGCAATGACATTAAG 432  
 Db 405 AACCTGCGGACCGAGAT-----CAGATGGGTGAAGATCTGACCGCGTGGATCGAG 458  
 Qy 433 CAACTGCGCGGTCTTGAAGCAAACTTTGGAAGACTCTTGAATTTGTTAGGCAATGAAG 492  
 Db 459 GACCTGCGGACCTTGAAGCAAAATGTCAGTCCGCTCTCAAGAGATTCCCGAGAGAG 518  
 Qy 493 TATCATGTATTCACCAAGCACTGACACTTACAAAGAAAGCTTAAAGCAAGGAA 552  
 Db 519 TATCATGTATTCACCAAGCACTGACACTTACAAAGAGGTGAAGCACTCCAGAG 578  
 Qy 553 ACTTACCGCGCTCTTAATACATGATGATGATGAAGAGAGAAATCCGAG 603  
 Db 579 GCATACAAAGATCTGACGAGAGCTGGTATGCGGAGAGACCGCGGTAC 629  
 RESULT 10  
 CA732396 605 bp mRNA linear EST 26-NOV-2002  
 LOCUS CA732396  
 DEFINITION w1p1c.pk005.m21 w1p1c Triticum aestivum cDNA clone w1p1c.pk005.m21 5' end, mRNA sequence.  
 ACCESSION CA732396  
 VERSION CA732396.1 GI:25547994  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.  
 REFERENCE 1 (bases 1 to 605)  
 Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Mao,G., Caraher,N. and Hanafey,M.K.  
 Dupont wheat cDNA Sequence  
 Unpublished (2002)  
 JOURNAL Contact: Scott V. Tingey  
 Crop Genetics  
 E. I. Dupont de Nemours and Company  
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302-631-2602  
 Fax: 302-631-2607  
 Email: Scott.V.Tingey@USA.dupont.com  
 Seq primer: M13.  
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 /note="Vector: pluescript SK+; Site\_1: EcoRI; Site\_2: XhoI; Wheat (Triticum aestivum, Hi line) lemma and palea"

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 Best Local Similarity 67.0%; Pred. No. 2.7e-46;  
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 Db 105 GAGATGGGAGGGGAGAGATGAGATTAAGCGGATCGAAGACGCAAAACAGGAGTG 164  
 Qy 133 ACATATTTTAAAGAGAGATTGGATCTGAAGAAAGCCCAAGAGCTCACTGTTCTGT 192  
 Db 165 ACCTACTCCAAGCGCGGTGCGGGATCATGAAGAGCGCGGAGCTCACGTCCTGCG 224  
 Qy 193 GATGTCAGGTCTCTCTCATCATGTTCTCAAGCAAGAGAGTTGGCTGATTAACGCGAC 252  
 Db 225 GACGCCAGGTGCGCATCATCATGTTCTCTCCACCGCAAGTACCAAGATTCTGACGC 284  
 Qy 253 CCCTTACTGATTAATTAAGGGATATATGAGAGGTACCAAGTTGTGACTGGAATGATCTA 312  
 Db 285 ACCGGACCGACATCAAGGGATCTTTGACCGCTACGAGCGCATGGGAGCCAGCGCTG 344  
 Qy 313 TGAATGCTCAAGTATGAAGATGCAAGATACGCTGAAGCATCTGAATGAGATTAAACCA 372

ORIGIN  
 Query Match 25.9%; Score 237.8; DB 6; Length 605;  
 Best Local Similarity 67.7%; Pred. No. 4.1e-46;  
 Matches 329; Conservative 0; Mismatches 157; Indels 0; Gaps 0;  
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 Db 111 GAGATGGGAGGGGAGAGATGAGATTAAGCGGATCGAAGACGCAAAACAGGAGTG 170  
 Qy 133 ACATATTTTAAAGAGAGATTGGATCTGAAGAAAGCCCAAGAGCTCACTGTTCTGT 192  
 Db 171 ACCTACTCCAAGCGCGGTGCGGGATCATGAAGAGCGCGGAGCTCACGTCCTGCG 230  
 Qy 193 GATGTCAGGTCTCTCTCATCATGTTCTCAAGCAAGAGAGTTGGCTGATTAACGCGAC 252

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Db      231 GAGGCCAGGTGCGCATCATCTCTCTCCACCGGCAAGTACCAAGATTCTGACG 290
Qy      253 CCTCTACTGATATTAAAGGGAATATAGAGATACCAAGTTGTACTGAAATGATCTA 312
Db      291 ACCGGACCGACATCAAGGGGATCTTTGACCGCTACAGAGCCATCGGACACCTTG 350
Qy      313 TGGATATGCTAGTATGAGAGATGAGAAATACGCTGAGCATCTGATGATTAACAA 372
Db      351 TGGATGAGCAGATATAGATATATGACCGCACCTGAGCATCTTCAAGACATCAATCG 410
Qy      373 AACCTGAGGAAGATATGAGAGAGAAAGGGAGAAATTTGAGGGCATGACATTAAG 432
Db      411 AACCTGGACCGACGATACAGGCAAAAGATGGTGAAGATCTGACGCGCTGAGTTGAG 470
Qy      433 CAACCTGCGGCTTTTGAAGCAACTTTGGAAGAGTCTTTGAAATTTGTAGGCATTAAG 492
Db      471 GAGCTGCGGACCTTTGAAACAAATGTCGATGCGCTCTCAAGAGGTCCCGGNNNAAG 530
Qy      493 TATCATGTATGCGCACACAACTGACACTTACAGAAAAGCTTAAAGACACAAGGAA 552
Db      531 TATCATGTATGACCAAGCAGACTGAAACCTACAGAAAGATGTAAGCATCTCCANMG 590
Qy      553 ACTTAC 558
Db      591 GCATAC 596

RESULT 11
BF291839      532 bp      mRNA      linear      EST 17-NOV-2000
LOCUS      WHE2204_E12_J24ZS Aegilops speltoides anther cDNA library Aegilops
DEFINITION      speltoides cDNA clone WHE2204_E12_J24, mRNA sequence.
ACCESSION      BF291839
VERSION      BF291839.1 GI:11222903
KEYWORDS      EST.
SOURCE      Aegilops speltoides
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
      Poidea; Triticeae; Aegilops.
REFERENCE      1 (bases 1 to 532)
AUTHORS      Akhunov, E., Anderson, O.D., Chao, S., Chin, A., Choi, D.W., Close, T.J.,
      Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Kianian, P., Lazo, G.R.,
      Miller, R., Otto, C., Rausch, C.J., Seaton, C.L., Simons, K., Tong, J.C.
      and Zhang, D.
TITLE      The structure and function of the expressed portion of the wheat
      genomes - Another cDNA library from Aegilops speltoides
JOURNAL      Contact: Olin Anderson
COMMENT      Unpublished (2000)
      US Department of Agriculture, Agriculture Research Service, Pacific
      West Area, Western Regional Research Center
      800 Buchanan Street, Albany, CA 94710, USA
      Tel: 5105595773
      Fax: 5105595818
      Email: oanderson@pw.usda.gov
      Sequence have been trimmed to remove vector sequence and low
      quality sequence with phred score less than 20
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      Location/Qualifiers
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        /dev_stage="Premeiotic anthers"
        /lab_host="E. coli SOLR"
        /clone_id="Aegilops speltoides anther cDNA library"
        /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
        Site 1: EcoRI; Site 2: XhoI; Plants were grown in a growth
        chamber at the University of California, Davis (Akhunov)."
  
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ORIGIN
Query Match      25.9%; Score 237.2; DB 2; Length 532;
Best Local Similarity 69.9%; Pred. No. 5,6e-46;
Matches 320; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

premeiotic anthers were harvested, total RNA and poly(A)
RNA were prepared, from each tissue and then pooled. A
cDNA library was made, and the cDNA clones were in vivo
excised to give Bluescript phagemids in the T7 Close lab
(Akhunov, Chin, Choi, Fenton, Kianian, Otto,
Simons, Zhang) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."

73  GAGATGGGAGGGGGAGATAGATTAATAAAGATAGAAATCCGACAAAGCAAGT 132
Db  75  GAGATGGGAGGGGGAGATAGATTAATAAAGATAGAAATCCGACAAAGCAAGT 134
Qy  133  ACATATTTTAAAGAGAGATGGATTAATCTGAAGAGCCAGAGCTCACTGTTCTGT 192
Db  135  ACCTACTCAAGGCGCGGTGCGGATCATGAAGAGCGCGGAGCTCACCGTCTGCG 194
Qy  193  GATGCTCAGGCTCTCTCATCATGTTTCTACAGACAGAAAGTTGGCTGATTAAGTCCAGC 252
Db  195  GACGCCAGAGTGGCCATCATGTTCTCTCCACCGGAAAGTACCAAGATTTGCGACG 254
Qy  253  CCTCTACTGATATTAAAGGAGATTAATGAGAGTACCAAGTGTGACTGAATGATCTA 312
Db  255  ACCGGACCGACATCAAGGGGATCTTTGACCGCTACAGACAGCCATCGGACACAGCTTG 314
Qy  313  TGGATATGCTCAGTATGAGAGATGACGAATACGCTGAAGCATCTGAATGATTAACAA 372
Db  315  TGGATGAGACAGATAGATGAATATGACGCCACGCTGAGCATCTCAAGACATCAATCGG 374
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Db  375  AACCTGCGACCGAGATCGAGCAAAAGATGGTGAAGATCTGACGCGCTGAGTTGCGAG 434
Qy  433  CAACCTGCGGCGTCTGAGCAAACTTTGAAGAAGTCTCTTAAGAATTTGAGGATGAAG 492
Db  435  GAGCTGCGGACCTTGAAGCAAAATGTCATGCCGCTCTTAAGAGAGTTGCCAGAGAAAG 494
Qy  493  TATCATGTATGCGCACACAACTGACACTTACAAAGA 530
Db  495  TATCATGTATGACCAAGCAGACTGAAACCTTCAAGAA 532

RESULT 12
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LOCUS      BL01N0528D01.b Endosperm_5 Zea mays cDNA, mRNA sequence.
DEFINITION      CD439730
ACCESSION      CD439730
VERSION      CD439730.1 GI:31355373
KEYWORDS      EST.
SOURCE      Zea mays
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
      clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 872)
AUTHORS      Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,
      Larkin, B., Beckett, P., and Messing, J.
TITLE      Characterization of the maize endosperm transcriptome and its
      comparison to the rice genome
JOURNAL      Genome Res. 14 (10), 1932-1937 (2004)
COMMENT      Contact: Lai, Jinheng
      Dr. Joachim Messing's lab
      Wakeman Institute, Rutgers University
      190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
      Tel: 732-445-3801
      Fax: 732-445-5735
      Email: jlai@wakeman.rutgers.edu
      Seq primer: T3.
  
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## FEATURES

source

Location/Qualifiers

1..872  
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## ORIGIN

Query Match 25.7%; Score 236; DB 6; Length 872;  
 Best Local Similarity 59.1%; Pred. No. 1.2e-45;  
 Matches 404; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

75 GATGGGAGGGGGAAGATAGATATAAAGATAGAAATCCGACGACGACGCAAGTTAC 134  
 142 GATGGGCGGGGAGATCGATGATCAAGCGATGAGAACGCCACCGCCAGGTGAC 201  
 135 ATATTCTAAGAGAGAGATTGGGATCTGAAAGAGCCAGAGCTCACTGTTCTGTGA 194  
 202 CTACTCCAGCGCCGCGGATCATGAAAGAGCGCGAGCTCACCGGTCTGTGCA 261  
 195 TGCTCAGGTCTCTCATCATGTTCTCAGACAGCAAGAAAGTTGGCTGATTACTGACGCC 254  
 262 CGCCAGGTGCGCATCATGTTCTCTCCACCGGAGATCCAGCATGTTCTGCAACC 321  
 255 CTCTACTGATTTAAGGGGATATATGAGAGTACCAAGTTGTGACTGAAATGATCATG 314  
 322 CGGACCGACATCAAGACATCTTTGACCGGTACCAAGGCCATCGGAGCAGCCCTATG 381  
 315 GAATGCTCAGTATGAGATGAGATGCAAGATACGCTGAGCATCTGATGATGATTAACAAA 374  
 382 GATCGACAGATATGAGATATGACGCGCAGCTGAGCATCTCAAGACATCAATCTGTGG 441  
 375 CTGAGAGAGAGATTTGAGAGAGAGAGAGAGAAATGAGAGGCATGACATTAAGCA 434  
 442 TCTGCGCAGAGATTAGGCAAGAGATGGGAGAGATCTGACATCTGACCTTGACGA 501  
 435 ACTGCGGGGCTTTAGCAAACTTTGAGAAAGTCTCTTAGAATTTTGGGCTATGAAAGTA 494  
 502 GCTGCGGGGCTCGAGCAAAACCTGACGCGGCTCTCAAGAGGTTGGCCATAGGAAGTA 561  
 495 TCATGTATGCGCACACAACTGACCTTACAGAAAAAGTTTAAAGCAAGAGGAAC 554  
 562 CCATGTATGACGACGACGACTGATTAACCTTACAGAAAAAGTTGAAGCACTGCGACGAGGC 621  
 555 TTACCGGCTTAAATACATGAATCGATATGAAAGAGAGAAATCCGAATACGTTTAA 614  
 622 GTACAGAACTGACGAGAGCTAGGATCGGAGAGACCGGCGTTGCGGTACGTGA 681  
 615 TGTAGAAAACAGAGTAGAATTTTAAATTCGATTCATGAGTGAATGAGTGTCTCA 674  
 682 CAACACGGGCGCGCGCTGCGCTGAGACGCGCGCGCGCGCGCGCGCGCGCGCC 741  
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 742 GGAATGATAGCCCTTCGCGCGTGTGCGCCAGCCAACTGACGCGCATGAGCTTACGG 801  
 735 ATCAATGATTTTACCTTTCATTA 758  
 802 CTTCCAGCACTTCGCGCTGAGCTA 825

## RESULT 13

AY109302 1273 bp mRNA linear HTC 17-OCT-2002  
 LOCUS Zea mays PC0139627 mRNA sequence.  
 DEFINITION Zea mays  
 ACCESSION AY109302  
 VERSION AY109302.1 GI:21212794  
 KEYWORDS HTC.  
 SOURCE Zea mays

## ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 1273)

## AUTHORS

Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., White, M.S.,

## TITLE

Arthur, L.W., Hanafey, M., Morgante, M., and Tingey, S.V.

## JOURNAL

Maize Mapping Project/DuPont Consensus Sequences for Design of

## REFERENCE

Unpublished (2002)

## AUTHORS

Coe, E.H.

## TITLE

Direct Submission

## JOURNAL

Submitted (25-APR-2002) Maize Mapping Project, University of

## COMMENT

Missouri, Columbia, MO 65211, USA  
 If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
 searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,  
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the  
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat  
 Schnable, Iowa State, then clones may be requested from ZmDB:  
 www.zmdb.iastate.edu.

## FEATURES

source

Location/Qualifiers

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/note="this sequence is part of a project of EBT

assemblies resulting from the application of public

contigs to seed DuPont contigs; this resource was

assembled by DuPont as part of a collaboration for the

overgo addressing of BACs in conjunction with the Maize

Mapping Project"

## ORIGIN

Query Match 25.7%; Score 236; DB 3; Length 1273;  
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 Matches 404; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

75 GATGGGAGGGGGAAGATAGATATAAAGATAGAAATCCGACGACGCAAGTTAC 134  
 146 GATGGGCGGGGAGATCGATGATCAAGCGATGAGAACGCCACCGCCAGGTGAC 205  
 135 ATATTCTAAGAGAGAGATTGGGATCTGAAAGAGCCAGAGCTCACTGTTCTGTGA 194  
 206 CTACTCCAGGCGCGGAGATCAGAAAGAGCGCGGAGCTCACCGGTCTGTGCA 265  
 195 TGCTCAGGTCTCTCATCATGTTCTCAAGACAGAAAGTTGCTGATTACTGACGCC 254  
 266 CGCCAGGTGCGCATCATGTTCTCTCCACCGGAGATCCAGCATGTTCTGACGCC 325  
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 375 CTGAGAGAGAGATTGAGAGAGAGAGAGAGAAATTTGAGGCGCATGACATTAAGCA 434  
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 506 GCTGCGGGGCTCGAGCAAAACCTGACGCGGCTCTCAAGAGGTTGGCCATAGGAAGTA 565  
 495 TCATGTATGCGCACACAACTGACCTTACAGAAAAAGTTTAAAGCAAGAGGAAC 554  
 566 CCATGTATGACGACGACGACTGATTAACCTTACAGAAAAAGTTGAAGCACTGCGACGAGGC 625

QY 555 TTACGCGCTTAATACATGAACTGATATGAAAGAGAAATCCGAACCTACGGTTTAA 614  
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 DB 686 CAACAGAGGCGCGCGGTGCGCTCGGACGCGCGGCGCGCGCTGGGCGCGCGCGCG 745  
 QY 675 GATGTTTCCCTTTAGGGTGTTCATCCGAATCAGCCCAATCTGCTTGTAGTTATGA 734  
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 QY 735 ATCACATGATCTTAAGCTTGCATA 758  
 DB 806 CTTCCACGACCTCCGCTGGGCTA 829

RESULT 14  
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 LOCUS wpalc.pk016.11 wpalc Triticum aestivum cDNA clone wpalc.pk016.11 5'  
 DEFINITION end, mRNA sequence.  
 ACCESSION CAS97172  
 VERSION CAS97172.1 GI:25149628  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 605)  
 Tingley,S.V., Moore,G., Griffiths,S., Powell,W., Mollers,P.,  
 Dolan,M., Hainey,C., Miao,G., Caraher,N. and Hanafey,M.K.  
 Dupont wheat cDNA sequence in collaboration with the John Innes  
 Center 1  
 Unpublished (2002)  
 JOURNAL Contact: Scott V. Tingley  
 COMMENT Crop Genetics  
 E. I. Dupont de Nemours and Company  
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302-631-2602  
 Fax: 302-631-2607  
 Email: Scott.V.Tingley@USA.dupont.com  
 Seq primer: M13.

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 /clone\_lib="wpalc"  
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 XhoI; wheat (Triticum aestivum) pre-meiotic anchors JIC"

ORIGIN  
 Query Match 25.4%; Score 232.6; DB 6; Length 605;  
 Best Local Similarity 66.0%; Pred. No. 7.3e-45;  
 Matches 344; Conservative 0; Mismatches 171; Indels 6; Gaps 1;

QY 73 GAATGGGGAGGGGGAAGATGAGATTAAGAAATCGAGCAACAGCAAGT 132  
 DB 83 GAATGGGGAGGGGGAAGATGAGATTAAGCGATTCAGAAACGCAAAACAGCAGT 142  
 QY 133 ACATATCTAAGAGAGAGATTGGGATCTAGTAAGAGCCAGAGACTCACTGTTCTGT 192  
 DB 143 ACCTACTCAAGCGCGCGGTGGGATCATGAGAGAGCCGCGAGCTCACCGTCTGC 202  
 QY 193 GATGCTCAGGTCTCTCATCATGTTCTCAAGCAAGAAAGTTGGCTGATTAAGT 252  
 DB 203 GAGCCCAAGGTGCGCATCATGTTCTCTCCACCGGCAAGTACAGAGATTCTGAGC 262

QY 253 CCTCTACTGATATTAAAGGATATATAGAGGTACAGAGTTGTGACTGSAATGATCTA 312  
 DB 263 ACCGCAACCGAATCAAGGGGATCTTTGACCGCTACAGAGCCATGCGGACAGCGCTG 322  
 QY 313 TGGAAATGCTCAGTATGAGAGATGCAAAATACGTTAGACATCTGAATGATTAACCA 372  
 DB 323 TGGATCGACATATAGAAATATGACAGCGACGCTGAGCCATCTCAAGGACATCAATCG 382  
 QY 373 AACCTGAGGAAGAAATTAAGAGAGAAAGGGGAGAAATGAGAGGACATGACATTAAG 432  
 DB 383 AACCTGCGACCGAAT-----CAGAGTGGGTGAAGATCTGACGCGCTGAGATTGCG 436  
 QY 433 CAATGCGCGGTCTTGAAGCAATTGGAAGAGTCTTTAGAAATTTAGAGCATTAAG 492  
 DB 437 GAGCTGCGGACCTTGAAGAAATGTGATGCGCGCTCTCAAGAGGTTGCCAGNNMAAG 496  
 DB 493 TATCATGTATGCGCACACAACTGACATTAACAAGAAAGCTTAAGCAAGGGA 552  
 QY 497 TATCATGTATGATCACACGACGACTGAACCTCAAGAAAGANNGTGAAGACATCCGNNNN 556  
 QY 553 ACTTACCGCGCTCTAATATGATGACTGATTAAGAAAGGA 593  
 DB 557 NCATACAAAGATCTGACAGAGAGCTGGGTATGCGGNGA 597

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 DEFINITION 018.5\_06\_a10, mRNA sequence.  
 ACCESSION AJ803128  
 VERSION AJ803128.1 GI:51118456  
 KEYWORDS EST.  
 SOURCE Antirrhinum majus (snapdragon)  
 ORGANISM Antirrhinum majus  
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamiales; Lamiales; Plantaginaceae; Antirrhineae;  
 Antirrhinum.  
 1 (bases 1 to 604)  
 Zachgo,S., Stueber,K., Saedler,H., Sommer,H. and Schwarz-Sommer,Z.  
 Antirrhinum EST collection  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Schwarz-Sommer Z  
 Molekulare Pflanzen-genetik  
 MPI fuer Zuechtungsfor-schung  
 Carl-von-Linne Weg 10, D-50829, Germany.  
 Location/Qualifiers  
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ORIGIN  
 Query Match 24.9%; Score 228; DB 1; Length 604;  
 Best Local Similarity 61.7%; Pred. No. 9.2e-44;  
 Matches 363; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 23 GAAGAGAGGGTTGAGAGACAGAGAAACAGGGGAGAGAGAGATGGGGA 82  
 DB 17 GAAGAAAGAGGTTGAATTAATTAAGTGAATAATTTCTATGAAAAAATTAAGATGGCTC 76  
 QY 83 GGGGAGAGATAGATTAAGATTAAGATTAAGATCCGACGAGAGCAAGTTACATATTCTA 142  
 DB 77 GTGGAGAGATCCAGATTAAGATTAAGATTAAGATCAAAATTAAGATTAATTCCA 136  
 QY 143 AGAGAGAGATTGGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 202  
 DB 137 AGAGAGAAATGGGCTGTTCAAAAGAGCTCATGAACTCATGTTCTTTGTGATGAAAAAG 196

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QY 203 TCTCTCATCATGTTCTCAAGACAGGAAAGTTGCGTATTAATCTGACCCCTTACTG 262
Db 197 TTTCGGTTATCATGATCTCAAGTACTCAGAGATTCAAGTATCATCAGCCCCCTCCATTA 256
QY 263 ATATTAGGGGATATATGAGAGGATCCAGGTTGTGACTGGAATGGATCTATGGAAATGTC 322
Db 257 CGACAAAGGAGTGTGTTGATTAAGTATCAACATGCTGTTGAGGTGATCTTTGGAAACAC 316
QY 323 AGTATGAGAGATGACAGATACGCTGAAGCATCTGAATGAGATTAAACCAAACTGAGGA 382
Db 317 ACTACGAGAAATGCAAGACATTTGAAGAGCTAAAGAGATTAAACAGGATCTCGGA 376
QY 383 AGGAGATTAGAGAGAGAGAGGAGGAATTGAGGCGATGACATTAAGCACTGCGG 442
Db 377 AGGAGATTAGGCAAAAGATGGAGAGATTGAAATGACATAGGCTACGAGCAAAATGTTA 436
QY 443 GTCTTGAGCAAACTTTGGAAGAGTCTCTTAGAATTGTTAGGCAATGAAGTATCATGTA 502
Db 437 ATTCATTTGAAGAAATTTGATTAATCTCTCAGGGTCAATTCGTAAAGAAAGTATTAAGTCA 496
QY 503 TCGCCACAAAATGACACTTACAAGAAAAAGCTTTAAAGCACAAGGAAAATTACCGCG 562
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Db 557 GCTTAATGCTGGAATATGATACATACAGGAGATCCACACTTTGGAT 604
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 10:07:00 ; Search time 202 Seconds  
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7428.048 Million cell updates/sec

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	216.6	23.6	989 4	US-09-640-211A-10
4	159.2	17.4	386 4	US-09-640-211A-2008
5	149.8	16.3	905 4	US-09-640-211A-1944
6	143.4	15.6	409 4	US-09-640-211A-1512
7	124	13.5	263 4	US-09-640-211A-1476
8	116	12.6	613 4	US-09-640-211A-2019
9	109.4	11.9	4285 3	US-09-410-464-1
10	109.2	11.9	412 4	US-09-640-211A-2031
11	105.8	11.5	396 4	US-09-640-211A-97
12	105.8	11.5	396 4	US-09-640-211A-1490
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14	102.8	11.2	684 4	US-09-640-211A-69
15	102.2	11.1	342 4	US-09-640-211A-12
16	102.2	11.1	356 4	US-09-640-211A-2017
17	101.8	11.1	1180 2	US-08-867-087B-16
18	101.2	11.0	5131 4	US-09-853-450-43
19	98.6	10.8	479 4	US-09-640-211A-350
20	98.6	10.8	479 4	US-09-640-211A-2091
21	98.4	10.7	945 2	US-08-485-981-9
22	98.4	10.7	945 2	US-08-867-087B-10
23	97.4	10.6	749 4	US-09-640-211A-361
24	97.4	10.6	749 4	US-09-640-211A-1980
25	96.8	10.6	1070 3	US-08-904-284-1
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27	96.6	10.5	1062 3	US-09-105-652-1

28	96.6	10.5	1062 3	US-09-349-677-1	Sequence 1, Appli
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32	95.4	10.4	5070 4	US-09-853-450-44	Sequence 44, Appli
33	95.4	10.4	5171 4	US-09-853-450-42	Sequence 42, Appli
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36	95	10.4	2437 3	US-08-904-284-6	Sequence 6, Appli
37	94.4	10.3	243 4	US-09-640-211A-368	Sequence 368, App
38	94.4	10.3	243 4	US-09-640-211A-1999	Sequence 1999, Ap
39	94.4	10.3	753 4	US-09-853-450-29	Sequence 29, Appli
40	93	10.1	663 4	US-09-853-450-37	Sequence 37, Appli
41	93	10.1	795 3	US-08-904-284-2	Sequence 2, Appli
42	92.2	10.1	423 4	US-09-640-211A-1463	Sequence 1463, Ap
43	92.2	10.1	706 4	US-09-640-211A-96	Sequence 96, Appli
44	91.8	10.0	1223 4	US-09-640-211A-32	Sequence 32, Appli
45	91.6	10.0	377 4	US-09-640-211A-1937	Sequence 1937, Ap

## ALIGNMENTS

RESULT 1  
US-09-410-464-2  
Sequence 2, Application US/09410464  
Patent No. 6395892  
GENERAL INFORMATION  
APPLICANT: Straus et al.  
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
TITLE OF INVENTION: poplar and other plant species.  
FILE REFERENCE: 53375  
CURRENT APPLICATION NUMBER: US/09/410,464  
CURRENT FILING DATE: 1999-10-01  
EARLIER APPLICATION NUMBER: 09/287,700  
EARLIER FILING DATE: 1999-04-06  
EARLIER APPLICATION NUMBER: 60/080,851  
EARLIER FILING DATE: 1998-04-06  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 946  
TYPE: DNA  
ORGANISM: Populus balsamifera subsp. trichocarpa  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (1)...(684)  
US-09-410-464-2

Query Match 24.9%; Score 228; DB 3; Length 946;  
Best local similarity 58.3%; Pred. No. 2.9e-52;  
Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY	76	ATGGGAGGGGAGATAGATATAAAGATGAGATCCGAGACAGGAGTTACA	135
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Qy 556 TACCGGCTCTAATATACATGAACTGATGATGAAAGAGAGAAATCCGAACTACGCTTTAAT 615
Db 481 CATGGAACCTCTTGATGAAATATGAGCAAACTAGAGATGACAGTATGCTTTAGTG 540
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Db 541 GACATGAGAGCTGCTGTTGACCTTGCAAAATGGGCTTCCAACCTCTATGATTCGCGCTG 600
Qy 676 ATGTTTCTTTAGAGGTTGTCATCCGAATCAGCCCAATCTGCTTGTTAGTTAGTAA 735
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Qy 736 TCACATGATCTTAGCCTTGCAATA 759
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## RESULT 2

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US-09-410-464-3
; Sequence 3, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; NAME/KEY: CDS
; LOCATION: (1)..(681)
US-09-410-464-3
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Query Match 24.8%; Score 227.2; DB 3; Length 681;

Best Local Similarity 58.4%; Pred. No. 4e-52; Mismatches 283; Indels 0; Gaps 0;

Matches 397; Conservative 0; Mismatches 283; Indels 0; Gaps 0;

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Qy 76 ATGGGAGGAGGAGATAGAGATAAAAGATAGAGATCCGAGCAAGGCAAGTTACA 135
Db 1 ATGGGTGTGGAAAGATTGAATCAAGAGATCGAAACCCCAAAACAGGCAAGTCACC 60
Qy 136 TATTTCAAGAGAGATTGGGATCTGAGAAAGGCCCAAGGCTCACTGTTCTTGAT 195
Db 61 TACTCGAAGAGAAATGTATTTTCAAGAAAGCCCAAGAACTCAGTGTATTTGAT 120
Qy 196 GCTAGAGTCTCTCATCATGTTCTCAAGCAGAGAAAGTGGCTGATTAAGAGCCC 255
Db 121 GCTAAGGCTCTCTTATCATGTTCTCAAGCAGTAACTCAATGAGTACATTAAGCCC 180
Qy 256 TCTACTGATATTAAGGAGATATAGAGGTACAGGTTGTGACTGGAATGATCTATGG 315
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Db 181 TCCACATCCACAAGAAAGATCTACATATATACAAACGCTTTAGGCATAGATCTGTGG 240
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Db 301 CTGAGACAGAAATCAGGCGAGAGAGAGAGGAGGCTTGAAATGATCTGAGCATTCAT 360
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Qy 496 CATGTATGCGCCACACAACTGACACTTACAGAAAAAGCTTTAAAGACACAGGAAACT 555
Db 421 CATGTATCAAAACACAAAAGAACTTACAGAAAGAGGTAAAGAAATTTAAGAGAGA 480
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Db 481 CATGGAACCTCTTGATGAAATATGAGCAAACTAGAGATGACAGTATGCTTTAGTG 540
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Qy 736 TCACATGATCTTAGCCTTGCA 755
Db 661 GCCCATGAACTTGCGCTTCTTGA 680
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## RESULT 3

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US-09-640-211A-10
; Sequence 10, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Modifications and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; EARLIER FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-10
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Query Match 23.6%; Score 216.6; DB 4; Length 969;

Best Local Similarity 64.4%; Pred. No. 3.8e-49; Mismatches 179; Indels 0; Gaps 0;

Matches 324; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

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Qy 73 GAGATGGGAGGAGGAGATAGAGATAAAAGATAGAGATCCGAGCAAGGCAAGTT 132
Db 4 GAGATGGGAGGAGGAGGAGATCCGAGTCAAGCTGATAGAGACACGAGCAAGGCGG 63
Qy 133 ACATATTCTAAGAGAGAGTGGGATCTGAAGAGGCCAAGGAGCTCACTGTTCTGT 192
Db 64 ACCTACTCGAAGGAGAGAGAGGCTCTTCAAGAAAGCGCAACGAGCTCAAGGCT 123
Qy 193 GATGCTCAGGTTCTCTCATCATGTTCTCAAGCAGAGCAAGAAAGTGGCTATTAAG 252
Db 124 GACCCCAAGGTTCTCATCATGATCTCAGCAGCGGAGAGCTCCAGAGTACATCAGC 183
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Db 483 CAAGGAACAATCTGTGTTAGCTAACAGAGATTAAAGAAAGCTGGAAGAGA 538

## RESULT 9

US-09-410-464-1  
; Sequence 1, Application US/09410464  
; Patent No. 6395892  
; GENERAL INFORMATION:  
; APPLICANT: Straus et al.  
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
; TITLE OF INVENTION: poplar and other plant species.  
; FILE REFERENCE: 53375  
; CURRENT APPLICATION NUMBER: US/09/410,464  
; CURRENT FILING DATE: 1999-10-01  
; EARLIER APPLICATION NUMBER: 09/287,700  
; EARLIER FILING DATE: 1999-04-06  
; EARLIER APPLICATION NUMBER: 60/080,851  
; EARLIER FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4285  
; TYPE: DNA  
; ORGANISM: Populus balsamifera subsp. trichocarpa  
US-09-410-464-1

Query Match 11.9%; Score 109.4; DB 3; Length 4285;  
Best Local Similarity 73.3%; Pred. No. 1.6e-19;  
Matches 140; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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Qy 130 GTTACATATTCTTAAGAGAGAGATTGGATCTGAAGAGCCCAAGAGCTCACTGTTCTC 189  
Db 2055 GTCACTTACTCGAAGAGAAATGATTTTCAAGAAAGCCCAAGAACTCACTGTTCTT 2114

Qy 190 TGTATGCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTACTGC 249  
Db 2115 TGTATGCTCAGGCTCTCTCTCATCATGTTCTCTCAACACTCAACAACTCAATGATCAATT 2174

Qy 250 AGCCCTCTAC 260  
Db 2175 AGCCCTCTCAC 2185

## RESULT 10

US-09-640-211A-2031  
; Sequence 2031, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; TITLE OF INVENTION: Modification of Gene Transcription  
; FILE REFERENCE: 11000.1021CIU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; CURRENT FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2031  
; LENGTH: 412  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-09-640-211A-2031

Query Match 11.9%; Score 109.2; DB 4; Length 412;  
Best Local Similarity 74.2%; Pred. No. 5.6e-20;  
Matches 138; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 70 AGAGAGATGGGGAGGGGAGATAGAGATMAAAAAGATAGAAATCCGACGACGAGCAA 129  
Db 130 AGGAAGATGGCGGAAAGAGAAAGATTAAGAAATAGACAACTTGACGGGAGGCGAG 189  
Qy 130 GTTACATATTCTTAAGAGAGAGATTGGATCTGAAGAGCCCAAGAGCTCACTGTTCTC 189  
Db 190 GTACATTTCTCGAAGAGAGAGAGAGGGCTGATCAAGAGGCCAGAGCTCTCCGTTCTG 249  
Qy 190 TGTATGCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTACTGC 249  
Db 250 TGTATGCTCAGGCTCTCTCATCATGTTCTCTCAAGCAGAGAAAGTTGGCTGATTACTGC 309  
Qy 250 AGCCCTC 255  
Db 310 AGCTCC 315

## RESULT 11

US-09-640-211A-97  
; Sequence 97, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; TITLE OF INVENTION: Modification of Gene Transcription  
; FILE REFERENCE: 11000.1021CIU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; CURRENT FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 396  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-09-640-211A-97

Query Match 11.5%; Score 105.8; DB 4; Length 396;  
Best Local Similarity 74.0%; Pred. No. 4.7e-19;  
Matches 134; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 71 GAGAGATGGGGAGGGGAGATAGAGATMAAAAAGATAGAAATCCGACGACGAGCAAG 130  
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Db 61 TTACATTTCTGAAAGAGCGTCTCTGCTCTCAAGAGGGGCGAGAGCTCTTATCTCT 120

Qy 191 GTATGCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTACTGCA 250  
Db 121 GTATGCTCAGGCTCTCTCATCATGTTCTCTCAAGCAGAGAAAGTTGGCTGATTACTGCA 180

Qy 251 G 251  
Db 181 G 181

## RESULT 12

US-09-640-211A-1490  
; Sequence 1490, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; TITLE OF INVENTION: Modification of Gene Transcription  
; FILE REFERENCE: 11000.1021CIU



Qy	128	AACTTACATATCTTAAGAGAGAGTTGGATCTGAAGAAAGCCCAAGAGCTCACTGTTT	187
Db	61	AGGTGACCTTCTCAAGAGAGAGATGGCTGTTGAAGAAAGGCTATGAGCTCTGTGTC	120
Qy	188	TCTGTATGCTCAGGCTCTCTCATATGTTTCAAGCACAGAAAGTTGGTGATTACT	247
Db	121	TGTGTATGTTGAGGTGCGGCTCTCATCTTCTCCAGCCGTTGCAAGCTCTATGAGTTTG	180
Qy	248	GCAAGCC 254	
Db	181	GCAAGCC 187	

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US10J\_PUBCOMB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US10K\_PUBCOMB.seq:\*  
23: /cgn2\_6/ptodata/1/pubpna/US10L\_PUBCOMB.seq:\*  
24: /cgn2\_6/ptodata/1/pubpna/US10M\_PUBCOMB.seq:\*  
25: /cgn2\_6/ptodata/1/pubpna/US10N\_PUBCOMB.seq:\*  
26: /cgn2\_6/ptodata/1/pubpna/US10O\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match Length	ID	Description
1	917	100.0	917	US-10-690-246-1
2	357.6	35.0	898	US-10-690-246-7
3	324.2	35.4	1036	US-10-690-246-5
4	316.8	34.5	980	US-10-690-246-3
5	245.2	26.7	637	US-10-487-901-7033
6	236	25.7	21	US-10-343-477A-45
7	234.8	25.6	681	US-10-260-238-5530

8	228	24.9	946	US-10-104-580-2	Sequence 2, Appli
9	227.2	24.8	681	US-10-104-580-3	Sequence 3, Appli
10	216.6	23.6	989	US-10-856-499-10	Sequence 10, Appli
11	215	23.4	644	US-10-021-323-8631	Sequence 8631, Ap
12	210.4	22.9	1036	US-10-424-599-120794	Sequence 120794,
13	209.8	22.9	664	US-10-487-901-3483	Sequence 3483, Ap
14	209.8	22.9	665	US-10-487-901-7018	Sequence 7018, Ap
15	207.2	22.6	926	US-10-343-477A-49	Sequence 49, Appl
16	203.4	22.2	630	US-10-487-901-7174	Sequence 7174, Ap
17	202	22.0	871	US-10-425-114-10670	Sequence 10670, A
18	201.2	21.9	498	US-09-732-627A-4479	Sequence 4479, Ap
19	198.4	21.6	1231	US-10-425-114-15025	Sequence 15025, A
20	192	20.9	1050	US-10-425-114-12758	Sequence 12758, A
21	190.6	20.8	1232	US-10-425-114-11957	Sequence 11957, A
22	187.4	20.4	1155	US-10-424-599-66649	Sequence 66649, A
23	176	19.2	425	US-09-922-293-14	Sequence 14, Appl
24	170	18.5	432	US-09-922-293-16	Sequence 16, Appl
25	169.4	18.5	933	US-10-424-599-33218	Sequence 33218, A
26	169.4	18.5	933	US-10-424-599-33218	Sequence 33218, A
27	168.2	18.3	2237	US-10-425-114-13190	Sequence 13190, A
28	168	18.3	401	US-09-922-293-13795	Sequence 13, Appl
29	167.4	18.3	2718	US-10-424-599-120795	Sequence 120795,
30	163.6	17.8	1007	US-10-425-114-14870	Sequence 14870, A
31	163.6	17.8	1021	US-10-424-599-65326	Sequence 65326, A
32	160.4	17.5	407	US-09-922-293-3394	Sequence 3294, Ap
33	159.6	17.4	964	US-10-739-930-33200	Sequence 3200, Ap
34	159.2	17.4	366	US-10-856-499-2008	Sequence 2008, Ap
35	155.2	16.9	360	US-09-922-293-15	Sequence 15, Appl
36	153.8	16.8	914	US-10-412-699B-55	Sequence 55, Appl
37	151.8	16.6	951	US-10-767-795-2121	Sequence 2121, Ap
38	151.2	16.5	886	US-10-278-536-238	Sequence 238, App
39	149.8	16.3	905	US-10-856-499-13444	Sequence 1344, Ap
40	148.6	16.2	474	US-09-732-627A-4667	Sequence 4667, Ap
41	148.2	16.0	639	US-10-021-323-8682	Sequence 8682, Ap
42	146.4	15.7	601	US-10-021-323-13542	Sequence 13542, A
43	145.6	15.9	742	US-10-487-901-3474	Sequence 3474, Ap
44	144.2	15.7	632	US-10-487-901-3376	Sequence 3376, Ap
45	143.4	15.6	499	US-10-856-499-1512	Sequence 1512, Ap

#### ALIGNMENTS

RESULT 1  
US-10-690-246-1  
; Sequence 1, Application US/10690246  
; Publication No. US20040210967A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEN, HONG-HUA  
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID  
; FILE REFERENCE: U 014863-8  
; CURRENT APPLICATION NUMBER: US/10/690,246  
; PRIOR FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: 091125320  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 917  
; TYPE: DNA  
; ORGANISM: Phalaenopsis equestris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (76)..(759)  
US-10-690-246-1

Query Match 100.0%; Score 917; DB 20; Length 917;  
Best Local Similarity 100.0%; Pred. No. 1e-231;  
Matches 917; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 ACGGGGATAGTAGAGGAAGAGGAGGTTGAGACAGAGAAACAGGGAGAA 60  
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Db      1 ACCGGGATAGTAGAGAGAGAGAGAGAGGGTTGAGAACAGAGAGAAACAGGGAGAA 60
QY      61 CAGGGGAGAGAGAGATGGGGAGGGAGAGTAGAGTAAAGATAGAGATCCGACG 120
Db      61 CAGGGGAGAGAGAGATGGGGAGGGAGAGTAGAGTAAAGATAGAGATCCGACG 120
QY      121 AACAGGCAAGTTACATATTTCTAAGAGAGAGATTGGATACGTAAAGAGCCAGAGCTC 180
Db      121 AACAGGCAAGTTACATATTTCTAAGAGAGAGATTGGATACGTAAAGAGCCAGAGCTC 180
QY      181 ACTGTTCTCTGTAGATGCTCAGGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCT 240
Db      181 ACTGTTCTCTGTAGATGCTCAGGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCT 240
QY      241 GATTACTGACAGCCCTCTACATATTAAGGGGATATATGAGAGGTACAGAGTTGTGACT 300
Db      241 GATTACTGACAGCCCTCTACATATTAAGGGGATATATGAGAGGTACAGAGTTGTGACT 300
QY      301 GGAATGATCTATGGAATGCTCAGTATGAGAGATGAGAAATCGCTGAAGCATCTGAAT 360
Db      301 GGAATGATCTATGGAATGCTCAGTATGAGAGATGAGAAATCGCTGAAGCATCTGAAT 360
QY      361 GAGATTACCAAAACCTGAGAGAGAGATTAGAGAGAGAGGGGAGAGAAATGGAGGC 420
Db      361 GAGATTACCAAAACCTGAGAGAGAGATTAGAGAGAGAGGGGAGAGAAATGGAGGC 420
QY      421 ATGGAACATAAGCAATCGCGGCTCTGAGCAAACTTTGGAAGATCTCTTAAATGTT 480
Db      421 ATGGAACATAAGCAATCGCGGCTCTGAGCAAACTTTGGAAGATCTCTTAAATGTT 480
QY      481 AGGATAGAAAGATATCATGTATGCGCACAAACCTGACCTTACAAAGAAAGCTTAA 540
Db      481 AGGATAGAAAGATATCATGTATGCGCACAAACCTGACCTTACAAAGAAAGCTTAA 540
QY      541 AGCACAAGGAAACTTACCGCGCTCTAATACATGATCGATATGAGAAAGAGAAATCCG 600
Db      541 AGCACAAGGAAACTTACCGCGCTCTAATACATGATCGATATGAGAAAGAGAAATCCG 600
QY      601 AACTAGGTTTATATGAGAAACAGAGTAGAATTTATGAAATTTGATTCAGATG 660
Db      601 AACTAGGTTTATATGAGAAACAGAGTAGAATTTATGAAATTTGATTCAGATG 660
QY      661 AATGAGTCTCAGATGTTTTCTTTAGGGTTGTTGATCCGATCAGCCCAATCTGCT 720
Db      661 AATGAGTCTCAGATGTTTTCTTTAGGGTTGTTGATCCGATCAGCCCAATCTGCT 720
QY      721 GGTTAGGTTATGATCATGATCTTACCTTGATATGAGAGATGATATATATGATTT 780
Db      721 GGTTAGGTTATGATCATGATCTTACCTTGATATGAGAGATGATATATATGATTT 780
QY      781 TATTTGATTTTATTTATGTTTAACTTTAGAAATTTATGAGAGGGGAGATCTATTCAGA 840
Db      781 TATTTGATTTTATTTATGTTTAACTTTAGAAATTTATGAGAGGGGAGATCTATTCAGA 840
QY      841 GAGAACTGCTTAAATTTGATTTCCGTTGTTGTTCTCTTCAATGTCAGTAAATTTT 900
Db      841 GAGAACTGCTTAAATTTGATTTCCGTTGTTGTTCTCTTCAATGTCAGTAAATTTT 900
QY      901 TTGTTTGTGTTTTTCGG 917
Db      901 TTGTTTGTGTTTTTCGG 917

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RESULT 2
US-10-690-246-7
; Sequence 7, Application US/10690246
; Publication No. US20040210967A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA
; APPLICANT: TSAI, MEN-CHIEH
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
; FILE REFERENCE: U 014863-8
; CURRENT APPLICATION NUMBER: US/10/690,246

```

```

; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 091125320
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Phalaenopsis equestris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (123)..(782)
US-10-690-246-7

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Query Match      39.0%; Score 357.6; DB 20; Length 898;
Best Local Similarity 75.7%; Pred. No. 8.5e-84;
Matches 457; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

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QY      76 ATGGGAGGGGAGAGATAGAGATTAAGAAAGATAGAGATCCGACGACAGGCAAGTTACA 135
Db      123 ATGGGAGAGGGAAGATAGAGATTAAGAAAGATAGAGATCCGACGAGCAAGTTACG 182
QY      136 TATTTCAAGAGAGATTGGGATCTGAGAGAGGCCAAGAGCTCATGTTCTGTGAT 195
Db      183 TATTTCAAGAGAGGACTTGGGATCTGAGAGAGGCCAAGAGCTCATGTTCTGTGAC 242
QY      196 GCTCAGGTCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTACTGACGCC 255
Db      243 GCTCAACTCTCACTATCATCTTCTCAAGCTCCGGAAAGTTAGCTGATTTCTGACGCC 302
QY      256 TCTACTGATTTAAGGGATATATGAGAGCTACAGGTTGTGATCTGAAATGATCTATGG 315
Db      303 TCCACAGAGGTTAAGATATATGTTGAGAGGTACCAAAATGTTACCGGAATGATATATGG 362
QY      316 AATGCTCAATAGAGAGATGAGATAGAGATAGCGCTGAAGCATCTGAATGATTAACCAAAAC 375
Db      363 GATGTCCAATATCAAGAGATGAGAACACTCTGAGAAATCTCAGGAGATTAATGTTAAT 422
QY      376 CTGAGAGAGAGATTTAGAGAGAGAGAGAGAGAAATGGAGGCTGAGCATTAAGCAAA 435
Db      423 CTTCAGAGAGAGATTAAGAGAGAGAGAGAGAGAAATCTGGAAGGTTGGGCTTTAAAGAG 482
QY      436 CTGCGGGCTCTTGAAGCAAACTTTGGAAGGCTCTTGAATGTTTGGCATAGAAATAT 495
Db      483 CTGCGGGCTCTTGAAGCAAAATTTGAGAGAGTGGTTAATGTTTGGCAGAGAAATGAT 542
QY      496 CATGTATGCGCCACAACTGACATCTTACAGAGAAAGCTTTAAAGCAACAGGGAAT 555
Db      543 CATGTATGCGCTTACGCAACAGACCTTGACAGAGAAAGCTTCAAAAGCAGACAAATA 602
QY      556 TACCGGCTCTAATAATCATGAACTGGATA--TGAAAGAGAGAAATCCGAATACGGTTTT 612
Db      603 TACAGAGCCCTTACGATGATCTGAGAGAGCTGAGAGAGAGATCAACCGTGAGTTTT 662
QY      613 AATGTAGAAACCAAGATAGAAATTTTGAAGATTCGATTCATAGTGTAATGATGCTCT 672
Db      663 CTGTGAGAGATCTAAGCTGATCTATGACAGCTCAATCTCAATGCAATGCGGCTGCAC 722
QY      673 CAGA 676
Db      723 CGGA 726

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RESULT 3
US-10-690-246-5
; Sequence 5, Application US/10690246
; Publication No. US20040210967A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA
; APPLICANT: TSAI, MEN-CHIEH
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
; FILE REFERENCE: U 014863-8
; CURRENT APPLICATION NUMBER: US/10/690,246

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: CURRENT FILING DATE: 2003-10-21
: PRIOR APPLICATION NUMBER: 091125320
: PRIOR FILING DATE: 2002-10-25
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 5
: LENGTH: 1036
: TYPE: DNA
: ORGANISM: Phalaenopsis equestris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (216)..(887)
US-10-690-246--5

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Query Match	35.4%	Score 324.2;	DB 20;	length 1036;
Best Local Similarity	69.1%;	Pred. No. 6.3e-75;		
Matches 475; Conservative	0;	Mismatches 203;	Indels 9;	Gaps 2;

OY	74	AGATGGGAGGGGGAAAGATAGATATAAAAAAGATGAGATATCCGACGAACGGCAAGTTA	133
Db	214	AGATGGGAGGGGGAAAGATAGATATAAAAAAGATGAGATATCCGATCGACTATCGGACAGTGA	273
OY	134	CATATTTAAAGAGAGAGTTGGGAATCTGAAGAAAGCCAGAGAGCTCACTGTTCTCTGTG	193
Db	274	CCTACTCCAAAGAGGAGAGCTGGGAATTAAGAAAGACGAGGAGATCACTGTTCTCTGTG	333
OY	194	ATGCTCAGAGTCTCTCATCATGTTCTCAAGCAAGAAAGTTGGCTGATTTACTGCAGCC	253
Db	334	ATGCTGAGGTTTCGTTATCATGTTCTCGAGATCTGGGAAGTTTCTGAGTACTGTAGCC	393
OY	254	CCTTACTGATATTAAAGGGATATATGAGAGGTACGAGGTTGACTGGAATGATCTAT	313
Db	394	CTTGCACGGAAACGAAGAGGTTTTCGAAACGCTACACAGAGGTATCTGGCATTTAATGTT	453
OY	314	GGAAATGCTCAGATATAGAGAGATGACGAATAGCCTGAAGCATGTAATGATTTAACAA	373
Db	454	GGAGCTGCAGATGACGAAGAGATGCTGATACGTTTACCATTCGAAAGAGATCAATCGCA	513
OY	374	ACCTGAGGAAGAGATTAGAGAGAGAAAGGGGAGAAATTGAGGGCATGACATPAAGC	433
Db	514	ATCTGAGGAGGGGAATGAAGCAGAGAGATGGGGGAAGATCTTGAGGGCATGATATCAAGG	573
OY	434	AACTGCGGGCTTTGAGCAAACTTTGGAAGACTCTTTGAATTGTGTGGCATTAAGAAAT	493
Db	574	AACTGCGGGCTTTGAGCAAACTTTGAAGAGCATTTGAAGCTTAGTACAAATATGAAGAAAT	633
OY	494	ATCATGTGATGCGCACACAAATGCACTTACAAAGAAAAAGCTTAAACCAAGGAA	553
Db	634	ATCATGTATNTACTGTACTCAACCGGACCTTACAAAGAAAGTTGAAGAACTCCCAAGAA	693
OY	554	CTTACCGCGCTTAAATACATGAACCTGGATATGAAGAAAGAGATCCGAATCGGTTTTA	613
Db	694	CACACCGGAATTATATGACGAATTTGAATCGTTGAGGACCAACCAAGTATAGGGTTCC	753
OY	614	ATGTGAAAAACAGATAGTAATTTATGAAATTTCAATTCATAGTGAATGATGTGCTC	673
Db	754	ACG-----AGGATTCAGCAATATGAGAGGGTGTCTTCTCTTGCAATATGACGGTCTC	807
OY	674	AGATGTTTTCTTTAGGGTGTTCATCCGAATCAGCCCAATCTGCTTGTGTTAAGTTATG	733
Db	808	ACATGATATCTTCCGG---GTGCAACCCACCAACAAATCTTCAAGGAACGGGATATA	864
OY	734	AATCAGATATCTTAGCCTTGCAATAT 760	
Db	865	GCTCTCAGATCTTGCCCTCGCTTGAT 891	

RESULT 4  
US-10-690-246-3  
; Sequence 3, Application US/10690246  
; Publication No. US20040210367A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEN, HONG-HWA

```

: APPLICANT: TSAI, MEN-CHIEH
: TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
: FILE REFERENCE: U 014863-8
: CURRENT APPLICATION NUMBER: US/10/690,246
: CURRENT FILING DATE: 2003-10-21
: PRIOR APPLICATION NUMBER: 091125320
: PRIOR FILING DATE: 2002-10-25
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 3
: LENGTH: 980
: TYPE: DNA
: ORGANISM: Phalaenopsis equestris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (196)..(864)
US-10-690-246-3

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Query Match	34.5%;	Score 316.8;	DB 20;	Length 980;
Best Local Similarity	65.3%;	Pred. No. 5.5e-73;		
Matches 503; Conservative	0;	Mismatches 252;	Indels 15;	Gaps 2;

QY	65	GGAAGAGAGAGATGGGAGGGGGAAAGTAAAGATAAAAAAAGATGAGAAATCCGCGAACA	124
Db	185	GAAAGAGAACCATGGGGAGGGGGAAAGATCGAGATAAAGAAATGGAAGACCTCTCAAAACA	244
QY	125	GGCAAGTTACATATTTCTAAGAGAGAGAGTTGGGATCTGAGAAAGGCCAAGAGACTGACTG	184
Db	245	GGCAGGTTACTTACTCTAAGAGAGAGGGGCTGGGATCATGAAMAAAGCCAGCGACTCCAGG	304
QY	185	TTCTCTGAGAGCTCAGGCTCTCTCATCATGTTCTGAAGCAGAGAAAGTTGGCTGATTT	244
Db	305	TTCTCTGAGAGCTCAGGCTCTCCCTGTTATGTTCTCGAGCACGGCGAAGTTCTCCGAGT	364
QY	245	ACTCAGAGCCCTCTACTGATATTTAAAGGGGATATATGAGAGTACCAAGTTTGACTGGAA	304
Db	365	ATTGTAGCTTACACCCGATACCAAGAGTGTATATGATTCGTTTACAGAGAGGTGTCGGGCA	424
QY	305	TGAGTCTATGGAATGCTCAGTATGAGAGAGATCGCAATACGCTGAGACTTGTAAATGAGA	364
Db	425	TAAATTTATGAGCGAGCAGCAGTACCAAGAAAGATGCAAGTAACCTTGAATCATTTGAAAGGA	484
QY	365	TTAAACCAAAACCTGAGAAAGAGATTTAGAGAGAGAAAGGGGAGAGAAATTTGAGGGCATGG	424
Db	485	TAAACCAAACTTGAAGGAGGAGATTAAGGCGAGAGATGGGCGAGAGTCTTGAAGGGCTAG	544
QY	425	AACATAAGCACTGGGGGCTTTGAGCAAACTTTTGAAGAGTCTCTTGAATTTGTTAGGC	484
Db	545	AAATTAAGAACTGGTGTGTCTTTGAGCAAAATATGAGCAGGGCCCTTAAGCTTTGTAAAGA	604
QY	485	ATGAAAGTATCATATGATTCGCCACACAAACCTGACACTTTCACAGAAAAAGCTTAAAGCA	544
Db	605	ATCGAAATATCATCGTATCATGACACCCAGACAGATTACTTCAAAAAAAAGTTGAAAAACT	664
QY	545	CAAGGAAACTTACCGCGCTCTAATACATGAACTGGAATATGAAAGAGAGAAATCCGAACCT	604
Db	665	CTCAAGAAACCCACAGAACTTACTCCGGGAGCT-----GGAAACTGAGCAGC	712
QY	605	ACGGTTTAAATGTGAAMAAACAGAGTAAATTTATGAAATTTCCATTCCAATGAGTAATG	664
Db	713	CCGTCTACTACGTGATGATGATTCACAAACAATGATGCGCGCTTGCACTTGAAGAAATG	772
QY	665	AGTGTCTCAGATGTTTTCTTTAGGGTGTTCATCCGAATCAGGCCAATCTGTGTGTT	724
Db	773	GGGCTTCCACTGTATTAATCAATTTGG---TACCACAAACAAAGCAGCGCAACTTCAGGGAG	829
QY	725	TAGGTTATGAAATCACATGATCTTAGCCTTGCAATATAGCAGATATATTAATGATTTTATTT	784
Db	830	TTGGATATGTCCCTCATGATCATCTACGCTCTCGGCTGATCTTTATATATTCGATGCCAACTG	889
QY	785	GAATTTTATTTATGTTGAACCTTTGAATTTATGAGATGGGGGATCTCA	834
Db	890	CTTAATATATCTATGATCTGATGTTCTTAAGCTTACAAAGTAGGGTCTTA	939

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RESULT 5
US-10-487-901-7033
; Sequence 7033, Application US/10487901
; Publication No. US2005091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreary, David
; APPLICANT: Bell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakelee, Beth
; APPLICANT: Larrina, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Confering Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; PRIORITY FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7033
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-7033
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Query Match          26.7%; Score 245.2; DB 21; Length 637;
Best Local Similarity 71.0%; Pred. No. 3.8e-54; Indels 0; Gaps 0;
Matches 325; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGGAAGATAGATATATAAAGATAGAGATCCGACGAAACAGGCAAGTTTACA 135
DB 180 ATGGGAGGGGGAAGATAGATATATAAAGATAGAGATCCGACGAAACAGGCAAGTTTACA 239
QY 136 TATTTAAGAGAGAGTTGGGATATGAGAGAGAGGCGCAAGAGCTCACTGTTCTGTGAT 195
DB 240 TACTCGAAGGCGCCGACGGGGATCATGAGAGAGCGCGAGGCTCACCGTCTCTCGAC 299
QY 196 GCTCAGGCTCTCTCATCATGTTCTCAAGCAAGGAAAGTTGGTGAATGATCTATG 255
DB 300 GCCCAGGTCGCAATCATGATGTTCTCTCCACGGGCAAGTACACGAGTTCTGAGCCCT 359
QY 256 TCTACTGATATTAAGGGATATATAGAGGTAACAGGTTGTGACTGGATGATCTATG 315
DB 360 TCCACCGACATCAAGGGGATTTTGACCGCTACAGCAAGGCAATCGGCAACAGCTTTGG 419
QY 316 AATGCTCAGTATGAGAGATGACAGATACGCTGAAGCATCTGAATGATTAACCAAAAC 375
DB 420 ATCAGCAGATATGAGATATGACAGCGCACGCTGAGCATCTCAAGGACATCAACCGAAC 479
QY 376 CTGAGGAAGAGATTAAGAGAGAGAGGGGAGGAATTGAGGCGCAGCATTAAGCA 435
DB 480 CTGGGACCGAGATCAGGCAAAAGATGAGAGAAAGATCTGAGCGGCTGAGTTGACAG 539
QY 436 CTGGCGGATCTTGAGCAAACTTTGGAAGAGTCTCTTGAATTTGTTAGGCAATAGAAATAT 495
DB 540 CTGGCGGATCTTGAGCAAAATGTCATGCGGCTTCAAGAGAGTTTCCGACAGGAATAT 599
QY 496 CATGTGATCGGCACACAACTGACATTTACAAAGAAAA 533
DB 600 CATGTGATCAGCACACAGACTGAACCTACAAAGAAAA 637
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RESULT 6
US-10-343-477A-45
; Sequence 45, Application US/10343477A
; Publication No. US2005065394A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Olga Danilevskaya
; APPLICANT: Pedro Hermon
; APPLICANT: Ed Bruggemann
; APPLICANT: David Shitroun
; APPLICANT: Evgenii Ananiev
; APPLICANT: J. Antoni Rafalski
; APPLICANT: Hajime Sakai
; APPLICANT: Edgar B. Cahoon
; APPLICANT: Rebecca E. Cahoon
; APPLICANT: Theodore M. Klein
; TITLE OF INVENTION: Floral Development Genes
; FILE REFERENCE: DD0014-PCT-USR
; CURRENT APPLICATION NUMBER: US/10/343,477A
; PRIORITY FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/253,415
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US01/43750
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Zea mays
US-10-343-477A-45
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Query Match          25.7%; Score 236; DB 21; Length 1257;
Best Local Similarity 59.1%; Pred. No. 1.5e-51; Indels 0; Gaps 0;
Matches 404; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

QY 75 GATGGGAGGGGGAAGATAGATATATAAAGATAGAGATCCGACGAAACAGGCAAGTTTAC 134
DB 130 GATGGGCGCGGGAAGATAGATCAAGGAGATCGAAGCGCAACCAACCGCAGAGTTAC 189
QY 135 ATATTTAAGAGAGAGTTGGGATATGAGAGAGAGGCGCAAGAGCTCACTGTTCTGTGTA 194
DB 190 CTACTCAGGCGCGGACCGGATCATGAGAGAGCGCGAGCTCACCGTCTCTGCGCA 249
QY 195 TGCTCAGGCTCTCTCATCATGTTCTCAAGCAAGGAAAGTTGGTGAATTAATGACGCC 254
DB 250 CGCCAGGTCGCAATCATGATGTTCTCTCCACCGGCAAGTACACAGATTTGACAGCCC 309
QY 255 CTCTACTGATATTAAGGGATATATAGAGGTAACAGGTTGTGACTGGAATGATCTATG 314
DB 310 CGGAACCGACATTAACATCTTTGACCGGTAACGACGAGCATCGGACCAAGCTTATG 369
QY 315 GAAATGCTCAGTATGAGAGATGACAGATACGCTGAAGCATCTGAATGATTAACCAAA 374
DB 370 GATCGAGCAGTATGAGATATGACAGCGCACGCTGAGCCATCTCAAGGACATCAATG 429
QY 375 CCGAAGAGAGGATTAAGAGAGAGAGGGGAGGAATTGAGGGCATGACATTAAGCA 434
DB 430 TTGCGCACAGAGATTAAGGCAAGATGAGGCGAGATCTGACAGTCTGACCTTGA 489
QY 435 ACTGCCGATCTTGAGCAAACTTTGGAAGAGTCTCTTGAATTTGTTAGGCAATAGAAATG 494
DB 490 GCTGCCGCGCTCGACCAAAAGTGAAGCGGCTCTCAAGAGAGTTTCCGCAATGAGAAATG 549
QY 495 TCATGTATCGGCACACAACTGACATTTACAAAGAAAAAGTTTAAAGCAAGGGAAC 554
DB 550 CCATGTATCAGCACACAGATGATCTTACAAAGAAAAAGTGAAGCAATCGCACAGGCG 609
QY 555 TTACCGCGCTTAAATCATGAACTGATATGAAAGAGGAGAAATCCGAATCAAGGTTTAA 614
DB 610 GTTCAAGAACTGACAGAGCTAGAGCATGCGGAGGACCCGCGCTTGAGGATGAGTGA 669
QY 615 TGTAGAAAAACAGAGATGAGATTTATGAAATTCGATTCGAATGATGATGATGCTCA 674
DB 670 CAACAGGGCGCGGCGTCTGAGGACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 729
QY 675 GATGTTTCTTTAGGGTGTTCATCGAATCAGCCCAATCTGCTTGTGTTAGTTATGA 734
```



Db 730 GGAATGATGACCTTCCGCTGCTGCGCCAGCCAGCCCAACTGACAGGCAATGCGCTTAACG 789  
QY 735 ATGACATGATCTTAAAGCTTGCATTA 758  
Db 790 CTTCCAGACACTCGCGCTGGGCTTA 813

RESULT 7  
US-10-260-238-5530

; Sequence 5530, Application US/10260238  
; Publication No. US20040016025A1  
; GENERAL INFORMATION:  
; APPLICANT: Budworth, Paul R.  
; APPLICANT: Moughamer, Todd G.  
; APPLICANT: Briggs, Steven P.  
; APPLICANT: Cooper, Bret  
; APPLICANT: Glazebrook, Jane  
; APPLICANT: Goff, Stephen A.  
; APPLICANT: Katagiri, Fumiyaki  
; APPLICANT: Kreps, Joel  
; APPLICANT: Provart, Nicholas  
; APPLICANT: Riecke, Darrell  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
; FILE REFERENCE: 60111-NP  
; CURRENT APPLICATION NUMBER: US/10/260,238  
; CURRENT FILING DATE: 2002-09-26  
; PRIOR APPLICATION NUMBER: US 60/325,448  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 60/325,277  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 60/370,620  
; PRIOR FILING DATE: 2002-04-04  
; NUMBER OF SEQ ID NOS: 6077  
; SEQ ID NO 5530  
; LENGTH: 681  
; TYPE: DNA  
; ORGANISM: Zea mays  
; US-10-260-238-5530

Query Match 25.6%; Score 234.8; DB 17; Length 681;  
Best Local Similarity 65.8%; Pred. No. 2.2e-51;  
Matches 341; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGGAAGATAGATTAATAAAGATAGATCCAGCAAGCAAGTTACA 135  
Db 1 ATGGGAGGGGGAAGATAGATTAATAAAGATAGATCCAGCAAGCAAGTTACA 60  
QY 136 TATTTCTAAGAGAGATTGGATCTGAAGAAAGCCAAAGAGCTCACTGTTCTGTGAT 195  
Db 61 TACTCAAGCCCGGACGGGATCATGAAGAGCGCGGAGCTCACCGTCTCTGCGAC 120  
QY 196 GCTCAGGCTCTCTCATATGATCTTCCAGCAAGCAAGAGTTGCTGAGAGCC 255  
Db 121 GCCCAGGCTGCGATCATATGATCTTCTCCACCGCAAGTACACAGATTTGAGGCC 180  
QY 256 TCTACTGATTTAAGGGGATATATGAGAGTACAGGTTGATGATGATGATGATG 315  
Db 181 GGAACCGATCAAGACATCTTTGACCGGTACAGAGCCATGAGGAGCCAGCTTAG 240  
QY 316 AATGCTCAGTATGAGAGATGAGATTAAGCTGAAGCATCTGAATGAGATTAACCAAAAC 375  
Db 241 ATCGAGCATATGAGATATGAGAGCGCAGCTGAGCCATCTCAAGACATCATGCTG 300  
QY 376 CTGAGGAAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435  
Db 301 CTGCGCAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
QY 436 CTGCGCGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495  
Db 361 CTGCGCGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
QY 496 CATGTGATGCGCAACAACTGACATTAACAAGAAAAGCTTTAAAGCAAGGAAACT 555

Db 421 CATGTGATGAGACCGAGACTGATACCTAACAAGAAAAGGTGAGACACTCGCAGGCG 480  
QY 556 TACCGCGCTTAAATACATGAACTGATGATGAAAGAGCA 593  
Db 481 TACAAGAACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 518

RESULT 8  
US-10-104-580-2

; Sequence 2, Application US/10104580  
; Publication No. US20030033628A1  
; GENERAL INFORMATION:  
; APPLICANT: Straus et al.  
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
; FILE REFERENCE: 62486  
; CURRENT APPLICATION NUMBER: US/10/104,580  
; CURRENT FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: 09/410,464  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 09/287,700  
; PRIOR FILING DATE: 1999-04-06  
; PRIOR APPLICATION NUMBER: 60/080,851  
; PRIOR FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 946  
; TYPE: DNA  
; ORGANISM: Populus balsamifera subsp. trichocarpa  
; NAME/KEY: CDS  
; LOCATION: (1) .. (684)  
US-10-104-580-2

Query Match 24.9%; Score 228; DB 14; Length 946;  
Best Local Similarity 58.3%; Pred. No. 1.6e-49;  
Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGGAAGATAGATTAATAAAGATAGAGATCCAGCAAGCAAGTTACA 135  
Db 1 ATGGGAGGGGGAAGATAGATTAATAAAGATAGAGATCCAGCAAGCAAGTTACA 60  
QY 136 TATTTCTAAGAGAGATTGGATCTGAAGAAAGCCAAAGAGCTCACTGTTCTGTGAT 195  
Db 61 TACTCAAGAGAGAAATGATATTTTCAAGAAAGCCCAAGAACTCACTGATCTTGTGAT 120  
QY 196 GCTCAGGCTCTCTCATATGATCTTCCAGCAAGCAAGAAAGTTGCTGATTAAGAGCC 255  
Db 121 GCTAAGGCTCTCTTATCATATGATCTTCCAGCAAGCAAGAAAGTTGCTGATTAAGAGCC 180  
QY 256 TCTACTGATTTAAGGGGATATATGAGAGTACAGGTTGATGATGATGATGATG 315  
Db 181 TCCATCAGCAAGAAAGATCTAGATCAATATCAGAAACCTTTAGGCAATGATCTGTG 240  
QY 316 AATGCTCAGTATGAGAGATGAGATTAAGCTGAAGCATCTGAATGAGATTAACCAAAAC 375  
Db 241 GGCACCTAATACGAGAAATGCAAGACACTTGGAGAGGCTGATGATGATTAATCAATCAAG 300  
QY 376 CTGAGGAAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435  
Db 301 CTGAGCAAGAGAACTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
QY 436 CTGCGCGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495  
Db 361 CTGCGCGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
QY 496 CATGTGATGCGCAACAACTGACATTAACAAGAAAAGCTTTAAAGCAAGGAAACT 555  
Db 421 CATGTGATCAAAAACAAAGAAAGCTTACAGAAAGAGAGAGAGAGAGAGAGAGAG 480  
QY 556 TACCGCGCTTAATACATGAACTGATATGAGAAAGAGAGAGAGAGAGAGAGAGAG 615

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Db      481 CATGAAACCTCTTGATGAAATATGAAAGCAAACTAGAGATGACGATATGGTTAGTG 540
Qy      616 GTAGAAAACCAAGTAGAATTTATGAAAATTCGATTCCATGGTAATGATGTCCTCAG 675
Db      541 GACAAATGAACTGCTGTGTGCACTTGCACAAATGGGGCTTCCAACTCTATGATCCGCTG 600
Qy      676 ATGTTTCCCTTGGGGTGTTCATCCGAATCAGCCCAATCGCTGTGGTTAGGTTATGA 735
Db      601 CATCAGGGGCAACAACCAACCATCTCCCTAATCTTCACTTGAGATGATTTGGA 660
Qy      736 TCACATGATCTTAGCCCTTGCAATTA 759
Db      661 GCCCATGAACTTGCCCTTCTTGA 684

RESULT 9
US-10-104-580-3
; Sequence 3, Application US/10104580
; Publication No. US20030033628A1
; GENERAL INFORMATION:
; APPLICANT: Straube et al.
; TITLE OF INVENTION: Floral, homeotic genes for manipulation of flowering in
; TITLE OF INVENTION: Poplar and other plant species.
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(681)
US-10-104-580-3

Query Match      24.8%; Score 227.2; DB 14; Length 681;
Best Local Similarity 58.4%; Pred. No. 2.2e-49;
Matches 397; Conservative 0; Mismatches 283; Indels 0; Gaps 0;

Qy      76 ATGGGAGGGGGAAGATAGATATAAAAGATAGAGAATCCGACGACGAGCAAGTTACA 135
Db      1 ATGGGCTGTGGAAGATTGAAATCAAGAAATGCGAAACCCCAAAACAGGCAAGTACC 60
Qy      136 TATTCTAAGAGAGAGTTGGATACCTGAAGAGGCCAAGAGCTCACTGTTCTGTGAT 195
Db      61 TACTCGAAGAGAAATGTAATTTTCAAGAAAGCCCAAGAACTCACTGATCTTGAT 120
Qy      196 GCTCAGGTTCTCTCATCATGTTTCTCAAGCAGAGAAAGTTGGTGTATCTGAGCCCC 255
Db      121 GCTAAGGTTCTCTTATCATGTTTCTCCAACTGAACCACTGAATGATCTTAAAGCCC 180
Qy      256 TCTACTGATATTAAAGGGATATATGAGAGTACCAAGTTGTTGACTGGAATGATCTTAAG 315
Db      181 TCCCATGACAAAGAAAGATTCAGATCAATATAGAAAGCTTTAGGCAATGATCTTGG 240
Qy      316 AATGCTCAGTAGAGAGATGACAGAAATACGCTGAAGCATCTGAATGAATTAACCAAAC 375
Db      241 GGCACTAATATGAGAAATGCAAGACACTTGAGAGAGCTGAATGATTAATCAATCATAG 300
Qy      376 CTGAGGAAGAGATTAGAGAGAGAGAGGGGAGAAATTTGAGGCACTGACATTAAGCA 435
Db      301 CTGAGCAAGAAATCAGGCAAGAGAGAGAGGGGCTTGAATGATCTGAGCATTTGATCAT 360
Qy      436 CTGGGCGGTCTTGAGCAAACTTTGAGAAAGTCTTGAATTTGTTAGGATAGAAAGTAT 495
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Db      361 CTGGGCGGTCTTGAGGACATATGACTGAAGCTTGAATGATGTCGTCGGCAGAAATGAC 420
Qy      496 CATGTATGCCACACAACTGACACTTTCAGAAAAAGCTTTAAAGCAAGGAAACT 555
Db      421 CATGTATGAAACAAACAAACCAAAACCTACAGAAAGAGTAAAGATTTAAGAGAGAA 480
Qy      556 TACCGGCTCTAATACATGAACTGATATGAAGAGAGAAATCCGAATCAGAGTTTAAAT 615
Db      481 CATGAAACCTCTTGATGAAATATGAGCAAACTAGAGATCGACAGTATGTTAGTG 540
Qy      616 GTAGAAAACCAAGTAGAATTTATGAAAATTCGATTCCAAATGTAATGATGTCCTCAG 675
Db      541 GACAAATGAACTGCTGTGTCACCTTGCAAAATGGGGCTTCCAACTCTATGATCCGCTG 600
Qy      676 ATGTTTCCCTTAGGGTGTTCATCCGAATCAGCCCAATCTGCTTGTGTTAGTTATGA 735
Db      601 CATCAGGGGCAACAACCAACCATCTCCCTAATCTTCACTTGAGATGATTTGGA 660
Qy      736 TCACATGATCTTAGCCCTTGCA 755
Db      661 GCCCATGAACTTGCCCTTCC 680

RESULT 10
US-10-856-499-10
; Sequence 10, Application US/10856499
; Publication No. US20040259145A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C2
; CURRENT APPLICATION NUMBER: US/10/856,499
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 2370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-856-499-10

Query Match      23.6%; Score 216.6; DB 20; Length 989;
Best Local Similarity 64.4%; Pred. No. 1.7e-46;
Matches 324; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy      73 GAGATGGGAGGGGGAAGATAGAGATAAAAGATGAGAAATCCGACGAACAGGCAAGTT 132
Db      4 GAGATGGGAGGGGGAAGATCCAGATCAAGCTGATAGAAACACGACGAACGGCAGGTG 63
Qy      133 ACATATTCTAAGAGAGAGTGGATCTGAAGATCTGAAGAGCCCAAGAGCTCATGTTCTGTG 192
Db      64 ACCTACTCGAAGAGAGAAAGCGGCTCTTCAAGAGGCAAGAGCTCACCGTCTTAAGG 123
Qy      193 GATGTCAGGTTCTCTCATCATGTTTCTCAAGCAGAGAAAGTTGGCTGATTAATCTGACG 252
Db      124 GACCCCAAGGTTCCATCATGATCTCCAGACCGGCAAGCTCCACAGATACATCAAC 183
Qy      253 CCTCTACTGATATTAAAGGGATATATGAGAGTACCAAGTTGTGACTGGAATGATCTTA 312
Db      184 CCTCCACCTCAACGAAGAGATGATGATCACTATCAACAGGCTTCAGGTTGATCTTC 243
Qy      313 TGAATGCTCAGTAGAGAGATGACAGAAATACGCTGAACATCTGAATGATTAACCAA 372
Db      244 TGAAGCTTCACTATAGAAAGATGCAAGAAACCTGAGGAAGCTGAAAGAGTGAACAA 303
Qy      373 AACCTGAGGAAGAGATTAGAGAGAAAGGGGAGAGAAATTTGAGGCACTGACATTAAG 432
Db      304 AACCTTCACTGAGAGGTCAGAGAGAGTTCCGGGAAAGACTGAATGATGATGAGCTTATCG 363
```

OY 433 CAATCGCGGCTTTCAGCAAACTTGGAAAGTCTTGAATTGTTAGCATTAAG 492  
DB 364 GAATTGGCGGCTTTCAGCAAACTTGGAAAGTCTTGAATTGTTAGCATTAAG 423  
OY 493 TATCATGTATGCGCAACAACCTTACCAAGAAAAGCTTAAGACACAAAGGAA 552  
DB 424 TACAAGACGCTCGGCAATCAATCGACCGCCAGGAAGAAAAGAAATGCTGAGSAA 483  
OY 553 ACTTACCGCGCTCTTAATACATGA 575  
DB 484 ATAAACAAAGTCTCTCGAAGA 506

## RESULT 11

US-10-021-323-8631  
; Sequence 8631, Application US/10021323  
; Publication No. US2004012334A1  
; GENERAL INFORMATION:  
; APPLICANT: Deikman, J11  
; APPLICANT: Feng, Paul C.C.  
; APPLICANT: Fincher, Karen L.  
; APPLICANT: Ziegler, Todd E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(52274)B  
; CURRENT APPLICATION NUMBER: US/10/021,323  
; CURRENT FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255, 619  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 17880  
; SEQ ID NO 8631  
; LENGTH: 644  
; TYPE: DNA  
; ORGANISM: Goseyplum hirsutum  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(644)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LHB3828-013-Q1-K6-F12  
US-10-021-323-8631

Query Match 23.4%; Score 215; DB 19; Length 644;  
Best Local Similarity 62.1%; Pred. No. 3.7e-46;  
Matches 338; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

OY 56 GAGAACGAGGAGAGAGATGGGAGGAGGAGATGAGATAAAGATAGATC 115  
DB 12 GAAAACTAGATTAATAATTAATGCTCGAGGAGAGATCAGATCAAGCTGATAGAACT 71  
OY 116 CGAGCAACAGGCAAGTATCATATTCTAAGAGAGATTGGATACCTGAAAGGCCAAG 175  
DB 72 CGACCAACAGGCAAGTATCATATTCTAAGAGAGATTGGATACCTGAAAGGCCAAG 131  
OY 176 AGCTCACTGTTCTGTGATGCTCAGTCTCTTCATCATGTTCTCAAGCAAGAAAGT 235  
DB 132 AACTTACAGTTCTTTCGATGCTAGAGTTTCATCATGTTCTCAAGCAAGAAAGT 191  
OY 236 TGGCTGATTACTGACAGCCCTCTACTATATTAAGGGATATATAGAGGTTACCAAGT 295  
DB 192 TCCATGATTTATACGCTTCCTACACAGAGCAAGTAATGATCACTACGAAAA 251  
OY 296 TGACTGATGATCTATGATATGCTCAGATGAGAGATGAGAAATGCTGAAAGATC 355  
DB 252 CTTGGGATGATGATCTGAGAACCCATATGAGAAATGAGAAAGCAAGTTGAAAGC 311  
OY 356 TGAATGATTAACCAAACTGAGAGAGAGATTGAGAGAGAGAGAGAGAGATTGG 415  
DB 312 TGAAGAAGATTAAACGAAAGCTGCGCAAGATTGAGAGAGAGAGAGAGATTGG 371  
OY 416 AGGGATGAGACATAAGCAAGTGGGCTTGAAGCAACTTGAAGAGTCTTTAGAA 475  
DB 372 ATGATTTAGACATGAAAGATCTTGGTCTTGAAGCAAGAAATGAGAGCTCTGACCTC 431

OY 476 TTGTTAGCATTAAGATATCATGATGCGCACAACTGACACTTACAGAAAAAGC 535  
DB 432 TTATTTGATTAAGAAATGATGTTCTCTCAACCAAGATTCATCTTACAGAAAAAG 491  
OY 536 TTAAGACCAAGGAACTTACCGGCTCTAATATCATGAACTGATATGAAAGAGAGA 595  
DB 492 TAGGAATGGAAGAGATACCAAAATCTTTATCATGAACTGGAATCCCTGAAGAG 551  
OY 596 ATCC 599  
DB 552 ATCC 555

## RESULT 12

US-10-424-599-120794  
; Sequence 120794, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 120794  
; LENGTH: 1036  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_80083C.1  
US-10-424-599-120794

Query Match 22.9%; Score 210.4; DB 18; Length 1036;  
Best Local Similarity 62.6%; Pred. No. 7.8e-45;  
Matches 328; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

OY 76 ATGGGAGGAGGAGATGATTAAGATTAAGATGAGATCCAGCAAGCAAGTTACA 135  
DB 27 ATGGCTGAGAGAAAGATCCAGATCAGAGATGAGAAACCAACCAAGCCAGTACT 86  
OY 136 TATTTAAGAGAGAGATTGGATATCTGAAGAGCCCAAGAGCTCACTGTTCTGTGAT 195  
DB 87 TATTTAAGAGAGAGATGCTCTTCAAGAGCCCAAGAGCTCACTGTTCTGTGAT 146  
OY 196 GCTCAGTCTCTCATCATGTTCTCAAGCAAGAAAGTTGGCTGATTCAGAGCCC 255  
DB 147 GCCAAGGTTTCTATTAATATGTTCTCCAGCACTGGGAAATCCACAGTCACTAGGCC 206  
OY 256 TCTACTGATTAAGGAGATATATGAGAGGATCAAGGTTGTAAGTGAATGATCTATG 315  
DB 207 TCACTCAACCAAGCAAGTTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 266  
OY 316 AATGCTAGATGAGAGATGAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 375  
DB 267 AACTCTATTAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 326  
OY 376 CTGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435  
DB 327 CTTGTAAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 386  
OY 436 CTGCGGAGTCTTGAAGAACTTGAAGAGTCTTGAAGATTTGTTAGCATTAAGAT 495  
DB 387 CTCAAGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 446  
OY 496 CATGTGATGCGCACAACTGACATTAAGAGAAAGCTTAAGAGAGAGAGAGAG 555  
DB 447 AAGGTATTAACAAATCAGATTAAGACCAAGAGAGAGAGAGAGAGAGAGAG 506

Qy 556 TACCGCGCTTAATACATGAGTGAATGAAAGAGAAATCC 599  
Db 507 CACAAACAGACTCTGTCAGTGAATGATCAAAAGCAGAAATCC 550

## RESULT 13

US-10-487-901-3483  
Sequence 3483, Application US/10487901  
Publication No. US20050091708A1  
GENERAL INFORMATION:  
APPLICANT: Oreido, Jeremiah Vincent  
APPLICANT: McCreery, David  
APPLICANT: Pell, Randy  
APPLICANT: Miller, Barbara  
APPLICANT: Weglarz, Thadeus  
APPLICANT: Gachotte, Daniel  
APPLICANT: Blakelee, Beth  
APPLICANT: Larrinua, Ignacio  
APPLICANT: Reddy, Avutu  
APPLICANT: Shukla, Vipula  
APPLICANT: Crosley, Rodney  
TITLE OF INVENTION: Nucleic Acid Compositions Confering Altered Metabolic Characteri  
FILE REFERENCE: DOM-08552  
CURRENT APPLICATION NUMBER: US/10/487,901  
CURRENT FILING DATE: 2004-02-26  
NUMBER OF SEQ ID NOS: 7560  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3483  
LENGTH: 664  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-487-901-3483

Query Match 22.9%; Score 209.8; DB 21; Length 664;  
Best Local Similarity 62.1%; Pred. No. 8.8e-45;  
Matches 331; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

Qy 76 ATGGGGAGGGGGAAGATAGATTAAGATTAAGAAATCCAGCAAGCAAGTTTACA 135  
Db 6 ATGGCGAGAGGGAAGATCCAGATCAGAGATAGAGAACGACAAACAGCAAGTACG 65  
Qy 136 TATTCTAAGAGAGAGTTGGATCTGAAGAGGCCAAGGACTCAGTTTCTGTGAT 195  
Db 66 TATTCAAGAGAAAGAAATGGTTTATTCAGAGAAACATGAGCTCAGCGTTTGTGTGAT 125  
Qy 196 GCTCAGGTCTCTCATCATGTTTCTCAAGCAGAGAAATGGCTGATTACTGAGCCCC 255  
Db 126 GCTAGGGTTTCATATCATGTTTCTTAAGCTCCAAACAAGCTTCAATGATATCAAGCCT 185  
Qy 256 TCTACTGATATTAAAGGGATATATGAGAGTACCAAGGTTGACTGGAATGATCTATG 315  
Db 186 AACACCAACAGAGAGATGTAGATCTGTACCAACTATTTCTGATGTCGATGTTGG 245  
Qy 316 AATGCTCAGTATGAGAGATGCAATACGCTGAAGATCTGATGATTAACCAAAAC 375  
Db 246 GCCACTCAATATGAGCGAATGCAAGAAACCAAGAGAAACGTGGAGACAAATAGAAAT 305  
Qy 376 CTGAGAGAGAGATTAGAGAGAGAGAGGAGGAATTGAGAGCATGACATTAAGCAA 435  
Db 306 CTGCGAGCTCAGATCAAGCAGAGAGCTAGTGAAGTGTGGAGCGACTTGAATCAAGAG 365  
Qy 436 CTGCGCGGCTTGAAGCAAACTTTGAAAGAGTCTCTTAAGATTTGTTAGCATAGAAAT 495  
Db 366 CTGCGTGTCTTGAAGTGAATGAAACCACTTCAAACTCGTTGCGAGCGCAAACTTC 425  
Qy 496 CATGTGATCGCAACAACCTGACACTTAACAAGAAAGCTTAAGACAAAGGAACT 555  
Db 426 AATCTCTTGGGAATCAGATCGAGCCACCAAGAAAGAAACAAAGTCAACAAGACATA 485  
Qy 556 TACCGCGCTTAATACATGAACTGATATGAAAGAGAGAAATCCGAATCAAG 608  
Db 556 TACCGCGCTTAATACATGAACTGATATGAAAGAGAGAAATCCGAATCAAG 608

Db 486 CAAAGATCTCATACATGAGCTGGAATTAAGAGTGAAGATCTCCTACTATG 538

## RESULT 14

US-10-487-901-7018  
Sequence 7018, Application US/10487901  
Publication No. US20050091708A1  
GENERAL INFORMATION:  
APPLICANT: Oreido, Jeremiah Vincent  
APPLICANT: McCreery, David  
APPLICANT: Pell, Randy  
APPLICANT: Miller, Barbara  
APPLICANT: Weglarz, Thadeus  
APPLICANT: Gachotte, Daniel  
APPLICANT: Blakelee, Beth  
APPLICANT: Larrinua, Ignacio  
APPLICANT: Reddy, Avutu  
APPLICANT: Shukla, Vipula  
APPLICANT: Crosley, Rodney  
TITLE OF INVENTION: Nucleic Acid Compositions Confering Altered Metabolic Characteri  
FILE REFERENCE: DOM-08552  
CURRENT APPLICATION NUMBER: US/10/487,901  
CURRENT FILING DATE: 2004-02-26  
NUMBER OF SEQ ID NOS: 7560  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7018  
LENGTH: 665  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-487-901-7018

Query Match 22.9%; Score 209.8; DB 21; Length 665;  
Best Local Similarity 62.1%; Pred. No. 8.8e-45;  
Matches 331; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

Qy 76 ATGGGGAGGGGGAAGATAGATTAAGATTAAGAAATCCAGCAAGCAAGTTTACA 135  
Db 6 ATGGCGAGAGGGAAGATCCAGATCAGAGATAGAGAACGACAAACAGCAAGTACG 65  
Qy 136 TATTCTAAGAGAGAGTTGGATCTGAAGAGGCCAAGGACTCAGTTTCTGTGAT 195  
Db 66 TATTCAAGAGAAAGAAATGGTTTATTCAGAGAAACATGAGCTCAGCGTTTGTGTGAT 125  
Qy 196 GCTCAGGTCTCTCATCATGTTTCTCAAGCAGAGAAATGGCTGATTACTGAGCCCC 255  
Db 126 GCTAGGGTTTCATATCATGTTTCTTAAGCTCCAAACAAGCTTCAATGATATCAAGCCT 185  
Qy 256 TCTACTGATATTAAAGGGATATATGAGAGTACCAAGGTTGACTGGAATGATCTATG 315  
Db 186 AACACCAACAGAGAGATGTAGATCTGTACCAACTATTTCTGATGTCGATGTTGG 245  
Qy 316 AATGCTCAGTATGAGAGATGCAATACGCTGAAGATCTGAATGATTAACCAAAAC 375  
Db 246 GCCACTCAATATGAGCGAATGCAAGAAACCAAGAGAAACGTGGAGACAAATAGAAAT 305  
Qy 376 CTGAGAGAGAGATTAGAGAGAGAGAGGAGGAATTGAGAGCATGACATTAAGCAA 435  
Db 306 CTGCGAGCTCAGATCAAGCAGAGAGCTAGTGAAGTGTGGAGCGACTTGAATCAAGAG 365  
Qy 436 CTGCGCGGCTTGAAGCAAACTTTGAAAGAGTCTCTTAAGATTTGTTAGCATAGAAAT 495  
Db 366 CTGCGTGTCTTGAAGTGAATGAAACCACTTCAAACTCGTTGCGAGCGCAAACTTC 425  
Qy 496 CATGTGATCGCAACAACCTGACACTTAACAAGAAAGCTTAAGACAAAGGAACT 555  
Db 426 AATCTCTTGGGAATCAGATCGAGCCACCAAGAAAGAAACAAAGTCAACAAGACATA 485  
Qy 556 TACCGCGCTTAATACATGAACTGATATGAAAGAGAGAAATCCGAATCAAG 608  
Db 486 CAAAGATCTCATACATGAGCTGGAATTAAGAGTGAAGATCTCCTACTATG 538

## RESULT 15

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US-10-343-477A-49
; Sequence 49, Application US/10343477A
; Publication No. US20050066394A1
; GENERAL INFORMATION:
; APPLICANT: Olga Danilevskaya
; APPLICANT: Pedro Hermon
; APPLICANT: Ed Bruggemann
; APPLICANT: David Shitroun
; APPLICANT: Evgenii Ananiev
; APPLICANT: J. Antoni Rafalski
; APPLICANT: Hajime Sakai
; APPLICANT: Edgar B. Cahoon
; APPLICANT: Rebecca E. Klein
; APPLICANT: Theodore M. Klein
; TITLE OF INVENTION: Floral Development Genes
; FILE REFERENCE: DD0014-PCT-USR
; CURRENT APPLICATION NUMBER: US/10/343,477A
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/253,415
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US01/43750
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Glycine max
US-10-343-477A-49
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Best Local Similarity 62.2%; Pred. No. 5,1e-44;
Matches 326; Conservative 0; Mismatches 198; Indels 0; Gaps 0;
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   |||||
QY 316 AATGCTCAGTATGAGAGATGAGATACGCTGAAGCATCTGAATGAGATTAAACCAAC 375
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Db 251 AACTCTATTAACGAAATATGCAAGAGAACTTGAAGAACTGAAGAGGTGAATAGAAAT 310
   |||||
QY 376 CTGAGAGAGAGATTAAGAGAGAGAGAGAGATTTGAGGCGCATGACATTAAGCAA 435
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Db 311 CTTCGTAAGAGATTAAGGAGAGATGAGAGATTGTCTGAACGAGCTGGGCGATGAAAGAT 370
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QY 436 CTGCGCGGCTTGAAGCAACTTTGAAAGTCTCTTGAATTTGAGCATAGAAAGTAT 495
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Db 371 CTCAAGCTCTTGAAGAGAAATGAGCAAGGCCGCCCAAGTTGTTCTGAGCGTAAAGTAT 430
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QY 496 CATGATTCGCAACAACTGACCTTAACAAAGAAAGCTTAAGCAAGAGAAACT 555
   |||||
Db 431 AAGGTATTAACAAATTCAGATTGACCCAGAGAGAAAGTTTAATTAACAGAGAAAGTGTG 490
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QY 556 TACCGCGCTTAATATACATGAATGAGATTAAGAGAGAGAAATCC 599
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Db 491 CACAAAGGCTCTGCAATGACTTGATGCAAAAGCAAGAAATCC 534
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Search completed: October 6, 2005, 13:00:19  
Job time : 831 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: October 6, 2005, 11:40:47 ; Search time 4399 Seconds

(without alignments)  
2500.417 Million cell updates/sec

Title: US-10-690-246A-2

Perfect score: 1177  
Sequence: 1 MGSKRIKIKIENPTNRQVT.....HPNPNLGIGYSHSLSLA 227

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US10690246/runat\_05102005\_110910\_6435/app\_query.fasta\_1.391  
-DB=genembl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR\_SCORE=pcc -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO MMAP -LARGESUBSTRY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

Genembl:\*  
1: gb ba:\*  
2: gb hcg:\*  
3: gb in:\*  
4: gb om:\*  
5: gb ov:\*  
6: gb pat:\*  
7: gb ph:\*  
8: gb pl:\*  
9: gb pr:\*  
10: gb ro:\*  
11: gb sts:\*  
12: gb sy:\*  
13: gb un:\*  
14: gb vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1177	100.0	910	8	AY378149 Phalaenop
2	820	69.7	952	8	AB094964 Asparaqus
3	802.5	68.2	1028	8	AY378147 Phalaenop
4	782.5	66.5	1005	8	AB071378 Lilium re

5	781.5	66.4	1039	8	AF503913	AF503913 Lilium lo
6	758.5	64.4	980	8	AY378150	AY378150 Phalaenop
7	755	64.1	1030	8	AY378148	AY378148 Phalaenop
8	738	62.7	833	8	AF209729	AF209729 Hemerocal
9	730.5	62.1	1002	8	AB094965	AB094965 Tulipa ge
10	716	60.8	942	8	AY196350	AY196350 Oncidium
11	701.5	59.6	1016	8	AB094966	AB094966 Tulipa ge
12	700	59.5	938	8	AF230706	AF230706 Tacca cha
13	684.5	58.2	1084	8	AB003323	AB003323 Oryza sat
14	684.5	58.2	1210	8	AK069317	AK069317 Oryza sat
15	682.5	58.0	830	8	AY621154	AY621154 Alpina h
16	675	57.3	1004	8	AF181479	AF181479 Zea mays
17	675	57.3	1257	6	CO855034	CO855034 Sequence
18	675	57.3	1257	6	AX478035	AX478035 Sequence
19	664	56.4	1061	8	AF077760	AF077760 Oryza sat
20	663	56.3	1166	8	AY541065	AY541065 Hordeum v
21	653	55.5	959	8	AB007506	AB007506 Triticum
22	651.5	55.4	852	8	AB050649	AB050649 Magnolia
23	642	54.5	1083	8	AB107993	AB107993 Triticum
24	641.5	54.5	830	8	AY397762	AY397762 Chloranth
25	633.5	53.8	651	8	AY337751	AY337751 Eupomatia
26	630.5	53.6	651	8	AY337750	AY337750 Eupomatia
27	630.5	53.6	1008	8	AF052874	AF052874 Papaver n
28	611	51.9	661	6	AR372459	AR372459 Sequence
29	611	51.9	946	6	AR372458	AR372458 Sequence
30	600.5	51.0	643	8	AY627631	AY627631 Akebia tr
31	588	50.0	643	8	TAB577377	TAB577377 Akebia tr
32	582	49.4	896	8	AY627630	AY627630 Akebia tr
33	579	49.2	809	8	AY436724	AY436724 Driymys wi
34	579	49.2	994	8	AF230704	AF230704 Petunia x
35	576	48.8	828	8	ACA419959	ACA419959 Asarum ca
36	574	48.8	851	8	AY436723	AY436723 Driymys wi
37	570	48.4	810	8	AY436725	AY436725 Driymys wi
38	567.5	48.2	852	8	AY436715	AY436715 Saruma he
39	565	48.0	906	6	GHY9724	GHY9724 Gerbera h
40	562	47.7	935	8	AY436736	AY436736 Lindera h
41	558	47.4	768	8	AY436722	AY436722 Driymys wi
42	557.5	47.4	926	6	CO855038	CO855038 Sequence
43	557.5	47.4	926	6	AX478039	AX478039 Sequence
44	556	47.2	807	8	AY436737	AY436737 Lindera e
45	555	47.2	834	8	ACA419955	ACA419955 Asarum ca

#### ALIGNMENTS

RESULT 1  
AY378149  
LOCUS  
DEFINITION Phalaenopsis equestris MADS box transcription factor (MADS2) mRNA, complete cds.  
ACCESSION AY378149.1 GI:38680584  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Phalaenopsis equestris  
Phalaenopsis equestris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Epidendroideae; higher Epidendroideae; Vandeeae; Aeridinae; Phalaenopsis.  
REFERENCE  
AUTHORS Tsai, W.C., Kuoh, C.S., Chuang, M.H., Chen, W.H. and Chen, H.H.  
TITLE Four DEF-like MADS Box Genes Displayed Distinct Floral Morphogenetic Roles in Phalaenopsis Orchid  
JOURNAL Plant Cell Physiol. 45 (7), 831-844 (2004)  
PUBMED 15295066  
REFERENCE  
2 (bases 1 to 910)  
AUTHORS Tsai, W.C., Chen, W.H. and Chen, H.H.  
TITLE Direct Submission  
JOURNAL Submitted (02-SEP-2003) Department of Biology, National Cheng Kung University, 1 University Rd., Tainan, Taiwan 701, Republic of China  
FEATURES  
source  
1..910  
/organism="Phalaenopsis equestris"





Oy		61 SerThraspiIeysgIlylIeyrgIuaXrTYgluValVaiPhrgIymeLapleTtp	80
Db		323 GGNCTTCACCCAAAGGCCATATTGTAATCGTTATCAGAACCTCACGGGAATCACTTGGS	382
Oy		81 AsnIagInTyrgIuaTgmEglnAsnThrLeuYshIsleubengIuleaInglnasn	100
Db		383 AGGCACAMATRTGAGAAAATCCAAAACAATGTAGAAGCATCTCAAGAGATCAACCAAC	442
Oy		101 LeuArgrIysgIuilearTarTargrIyGlgIugIuleugIuleugIyleMetAepIIeysgIn	120
Db		443 CTCGGCAAAGAAATCAGCAGAGAACGGGTGAAGACTTGATGGCATTCAGCAATCGAGAA	502
Oy		121 LeuArgrIyLeugIugInThrLeugIugIusertleuArgrIleValaRghIsatrylsTr	140
Db		503 CTGGCGCGGTCTTGAGCAAAATCTGGATGAAGCTGTAAAGCTGTTCGTCAACCGGAATAT	562
Oy		141 HisValIlealTaThrgInThrAspThrTyrlsYhsylsleuYseSerThrArgIuThr	160
Db		563 CATTTTATMGACGCGACAGATACCTTACAGAAAAAGTTGAAGCACTCCCAAGAAACA	622
Oy		161 TyzArghIaleuIleHsgIuleuaspMeIySgIugIusInProasnyTyrgIyPheasn	180
Db		623 CACAGAGATTTCGTCGCGATCTGATATGAAAGATGAGCATCAGATAACGGTTTTGTG	682
Oy		181 ValGIuabngInserrArgrIleTyrgIuanserIleProMetValaIngIucyProglu	200
Db		683 GATTAAGATCCMACCAAC--TATGAAGGTGTGCTGTCTGGCAAAATGGGGATCCCAAC	739
Oy		201 MetPheserPheaTgyValIHsProabngInProasnlleuLeugIyleugIyTyrgIu	220
Db		740 GTTAGCGATTTCGG--GTTCMAACCAAGTCAAGCCAANTCTCCACGHAATGGATGGCGT	796
Oy		221 SerHisApLeuSerLeuAla	227
Db		797 CCCATGATCTCCGCTTGA	817
RESULT 3			
LOCUS	AY378147	1028 bp	mRNA linear PLN 09-AUG-2004
DEFINITION	Phalaenopsis equestris MADS box transcription factor (MADS4) mRNA,		
	complete cds.		
ACCESSION	AY378147		
VERSION	AY378147.1	GI:38680577	
KEYWORDS			
SOURCE			
ORGANISM			
	Phalaenopsis equestris		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;		
	Epiphytoidae; higher Epiphytoidae; Vandaceae; Aroidae;		
	Phalaenopsis.		
REFERENCE	1 (bases 1 to 1028)		
AUTHORS	Tsai,W.C., Kuo,H.C.S., Chuang,M.H., Chen,W.H. and Chen,H.H.		
TITLE	Four DFR-like MADS Box Genes Displayed Distinct Floral		
JOURNAL	Morphogenetic Roles in Phalaenopsis Orchid		
PUBMED	Plant Cell Physiol. 45 (7), 831-844 (2004)		
REFERENCE	2 (bases 1 to 1028)		
AUTHORS	Tsai,W.C., Chen,W.H. and Chen,H.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-SEP-2003) Department of Biology, National Cheng Kung		
	University, 1 University Rd., Tainan, Taiwan 701, Republic of China		
FEATURES	Location/Qualifiers		
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QY	21 TyrSerIysArgArgValGlyIleLeuValAlaIleGluLeuThrValIleCysAsp	40					
Db	268 TACTCGAAGGAGAGCGTGGGATTTATCAAAAGCCGAGAGATCACTGTTCTCGCAT	327					
QY	41 AlaGlnValSerLeuIleMetPheSerSerThrGlyIleValLeuAlaAspIleCysSerPro	60					
Db	328 GCTGAGGTTTCGCTTATCATGTTCTCGAGTACGGGAACTTTCTGAGTCTGAGCCCT	387					
QY	61 SerThrAspIleIleGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr	80					
Db	388 TCGACGGAACGAAAGAGTTTGTGAACGCTACACAGGATCTGGCATTAATTGTGG	447					
QY	81 AsnAlaGlnIleTyrGluArgMetGlnAsnThrLeuIleValIleAsnGlnIleAsnGln	100					
Db	448 AGCTCGCAGTACGAAAGATGCTGATATCGCTTACCATTCGAAAGAGATCAATCGCAT	507					
QY	101 LeuArgIleGluIleArgArgTyrGlyGluIleGluIleGluIleGluIleGluIleGluIle	120					
Db	508 CTGACGAGGAGATGAGGAGAGAGATGCGGGAGATCTTGAGGGAGTATATCAAGAA	567					
QY	121 LeuArgIleGluIleGluIleThrLeuGluIleGluIleSerLeuArgIleValArgHisArgGlyTyr	140					
Db	568 CTGCGCGGCTTTGAGCAAAACATTGAGAGGCAATTGAACTGATACAAATATGAAATAT	627					
QY	141 HisValIleIleAlaThrGlnThrAspThrTyrIleValIleValIleValIleValIleValIle	160					
Db	628 CATTAATCACTACTCAACGAGACCTTCAAGAAAGAGTTGAAAGAACTCCCAAGAAACA	687					
QY	161 TyrArgAlaLeuIleHisGluLeuAspMetIleGluIleGluIleGluIleGluIleGluIle	180					
Db	688 CACCGGAACCTTAATGACGAGATTCGAATGCGATGAGGACCAACCGAGTATGAGGTTCCAC	747					
QY	181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValIleGluIleCysProGln	200					
Db	748 GAGATTCAACAACTATGAGAGGTTCTTCTGCTTGGAAATGACGAGTCTCAC	801					
QY	201 MetPheSerPheArgValValHisProAsnGlnProAsnLeuIleGluIleGlyTyrGlu	220					
Db	802 ATGATGCTTCCGCG--GTGCAACCCACCAACCAAAATCTTCAGAGGAGCGGATATATGC	858					
QY	221 SerHisAspLeuSerLeuAla	227					
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RESULT 4	ABO71378	1005 bp	mrna	linear	PLN 09-MAY-2002		
LOCUS	Lilium regale LRDBF	mrna	for MADS-box	transcription factor,			
DEFINITION	complete cds.						

ACCESSION AB071378  
VERSION AB071378.1 GI:20513259  
KEYWORDS  
SOURCE  
ORGANISM  
Lilium regale  
Lilium regale  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;  
Lilium.  
REFERENCE  
1  
AUTHORS  
Winter, K. U., Weiser, C., Kaufmann, K., Bohne, A., Kirchner, C.,  
Kanno, A., Saedler, H. and Theissen, G.  
TITLE  
Evolution of class B floral homeotic proteins: obligate  
heterodimerization originated from homodimerization  
JOURNAL  
Mol. Biol. Evol. 19 (5), 587-596 (2002)  
MEDLINE  
21959322  
PUBMED  
11961093  
REFERENCE  
2 (bases 1 to 1005)  
AUTHORS  
Kanno, A., Bohne, A., Saedler, H. and Theissen, G.  
TITLE  
Direct Submission  
Submitted (11-SEP-2001) Akira Kanno, Tohoku University, Graduate  
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi  
980-8577, Japan (E-mail: kanno@ise.tohoku.ac.jp,  
Tel: 81-22-217-5725 (ex. 5725), Fax: 81-22-217-5725)  
FEATURES  
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Alignment Scores:  
Pred. No.: 4.59e-63 Length: 1005  
Score: 782.50 Matches: 149  
Percent Similarity: 83.04% Conservative: 42  
Best Local Similarity: 64.78% Mismatches: 34  
Query Match: 66.48% Indels: 5  
DB: Gaps: 3  
US-10-690-246a-2 (1-227) x AB071378 (1-1005)  
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DB 10 ATGGGGGGGGGAAGATCGAGATTAAQAAGATCGAAAACTCGACGAATCGACAGTACT 69  
QY 21 TySerLyBArGArGValGlyIleLeuLySleValAlaYsgIuLeuThrValLeuCyAsp 40  
DB 70 TACCGAAGCGCCGACCGGAATCATCAAGAAGCGACTGAGCTCACTGCTGTGAT 129  
QY 41 AlAGlnValSerLeuIleMetPheSerSerThrGlyLySleuAlaAspTyCySerPro 60  
DB 130 GCCCAGGCTCTCTCCCTATGTTCTCCAGCACC GGGAAGCTGTCCAGAGTTCTCGACGCC 189  
QY 61 SerThraPliLeYsGlyIleTyrgIuArGlyrGlnValValThngIYmeCAspLeuTrp 80  
DB 190 TTCACACACACGAAGAAAGATCTTCACCGCTACCAAGACGCTGCGGAACTAACCTCTG 249  
QY 81 AsnAlaGlnTyrgIuArGmeGlnAaenThrLeuYshIleuAaGlnIleAaGlnAa 100  
DB 250 AGCCGCAATACGAAGAAATGCAAAACACTTGAACATCTGACGAGATCAACCGCAC 309

QY 101 LeuArGlyeGluIleArGArGlyeGlyGluGluGluYmeAspIleYsGln 120  
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DB 370 CTCGCGGCTTGAAGCAAAATTTGACGAGCGCTCAACCTGCTGCTACAGAAATAT 429  
QY 141 HisValIleAlaThrcIlnThraPliLeYsYleYsYleValSerThrArGlnThr 160  
DB 430 CAGTATATCAACACTGACAGACACTTACAAAGAAAGCTGCAAAAGCTGGAAGACA 489  
QY 161 TyrArAlaLeuIleHisGluLeu-----AspMeTyeGluGluAenProAenTy 177  
DB 490 CACAAAGACTTGCTCCGTGACCTCGTGATAGAGATTAAGATCAAGATCAAGCTAT 549  
QY 178 GlyPheAaValGluAaGlnSerArGlyeTyrgIuAaenSerIleProMeValaGln 197  
DB 550 GGTATGTAGACGAAGACCCAGCAAC--TATGATGGCGGCTTGTCTGCGCAATGG 606  
QY 198 CySProGlnMeCpHeSerPheArGValValHisProAaGlnProAaenLeuGlyLeu 217  
DB 607 GCTTCTCATCTGTACAGATTCCGA--GTCCAACGAGCCAGCCAACTGATGGGATG 663  
QY 218 GLYTYrGlyuSerHisAspLeuSerLeuAla 227  
DB 664 GGTTATGTTCCACGATCTCCGACTGGCT 693  
RESULT 5  
AF503913 1039 bp mRNA linear PLN 13-MAY-2002  
LOCUS  
Lilium longiflorum MADS box protein (MADS1) mRNA, complete cds.  
DEFINITION  
AF503913  
ACCESSION  
AF503913.1 GI:20531752  
KEYWORDS  
Lilium longiflorum (Trumpet Lily)  
Lilium longiflorum  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;  
Lilium.  
REFERENCE  
1 (bases 1 to 1039)  
AUTHORS  
Tzeng, T.-Y. and Yang, C.-H.  
TITLE  
A MADS box gene from lily (Lilium longiflorum) is sufficient to  
generate dominant negative mutation by interacting with PISTILLATA  
JOURNAL  
Plant Cell Physiol. 42 (10), 1156-1168 (2001)  
MEDLINE  
21530302  
PUBMED  
11673632  
REFERENCE  
2 (bases 1 to 1039)  
AUTHORS  
Tzeng, T.-Y. and Yang, C.-H.  
TITLE  
Direct Submission  
Submitted (18-APR-2002) Institute of Biotechnology, National Chung  
Hsing University, 250 Kao-Kung Rd., Taichung, Taiwan 40227, ROC  
FEATURES  
source  
1. .1039  
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16. .702  
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/product="MADS box protein"  
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/translation="MGRGKIEIKIENSTNROYTSKRRTGIKKATELVLCDAEVS  
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KETISQRMGEELDGLDKIDRLGLEONDEALKVHRKXHYINTQETRYKKKYNSEEA  
HNKILDLVNRKMDENPVYGYVDEPDSNYDGLALANGASHLYEFRRVQSPNHLGM  
GYGSHDLRLA"

## ORIGIN

## Alignment Scores:

Prod. No.: 5,9e-63 Length: 1039  
 Score: 781.50 Matches: 149  
 Percent Similarity: 83.04% Conservative: 42  
 Best Local Similarity: 64.78% Mismatches: 34  
 Query Match: 66.40% Indels: 5  
 Gaps: 3

US-10-690-246a-2 (1-227) x AF503913 (1-1039)

QY 1 MetGlyArgGlyLeuIleGluIleValSerIleGluAsnProThrAsnArgGlnValThr 20  
 DB 16 ATGGGCGGGGAAAGATCGAGATTAGAGATTCAGAACTCGACGAATCCGCGAGTCACT 75  
 QY 21 TyrSerIleValArgValAlaGlyIleLeuIleValSerIleValSerIleValSerIleValSer 40  
 DB 76 TACTCGAAGCGCGGACCGGACGATCATCAAGAGCGAGTGAAGTCTGAGTCTGAGT 135  
 QY 41 AlaGlnValSerIleValSerIleValSerIleValSerIleValSerIleValSerIleValSer 60  
 DB 136 GCGGAGGTCTCTCTCTTATGTTCTCCAGCACCGGAAAGCTGTCAAGATTCTGAGGCC 195  
 QY 61 SerThrApilIleValSerIleValSerIleValSerIleValSerIleValSerIleValSer 80  
 DB 196 TCCACAGACAGAGAGATCTTCGACCGCTACAGAGAGCTGTCCGGGATCAACCTCTGG 255  
 QY 81 AsnAlaGlnValSerIleValSerIleValSerIleValSerIleValSerIleValSerIleValSer 100  
 DB 256 AGCCGCGAATACGAGAAATGCAAAACCTTGAACCATCTGACCGAGATCAATCGCAC 315  
 QY 101 LeuArgIleValSerIleValSerIleValSerIleValSerIleValSerIleValSerIleValSer 120  
 DB 316 CTTCGCAAGAGATCAAGCAGAGATGCGGAGAGCTGATGATGATGATGATGATGATGATGAT 375  
 QY 121 LeuArgIleValSerIleValSerIleValSerIleValSerIleValSerIleValSerIleValSer 140  
 DB 376 CTGCGCGGTCTTGAAGAAATTTGAGACGACGCTCAAGCTGTCTGCTCAACCGGAGATGAT 435  
 QY 141 HisValIleAlaThrGlnThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 160  
 DB 436 CATGTGATGACACTCTCAGACAGACCTTACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGCA 495  
 QY 161 TyrArgAlaLeuIleHisGluLeu-----AspMetIleValSerIleValSerIleValSerIleValSer 177  
 DB 496 CACAGAACTTGTCTCGGACCTGTGTAATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 555  
 QY 178 GlyPheAsnValGluAsnGlnSerArgIleTyrGluAsnSerIlePheMetValAsnGlu 197  
 DB 556 GGTATATGAGACGAAACCCAGCAAC---TATGATGCGCGGCTGTGCTGCGCAATGGG 612  
 QY 198 CysProGlnMetPheSerPheArgValAlaHisProAsnGlnProAsnLeuIleGlu 217  
 DB 613 GCTTCTCATCTGTACGAGCTTCCGA---GTCCAAACCGACGACCAACCTGCATGGGATGG 669  
 QY 218 GlyTyrGluSerHisAspLeuSerLeuAla 227  
 DB 670 GGTATGAGCTCCCATGATCTCCGACTGGCT 699

RESULT 6  
 AY378150 980 bp mRNA linear PLN 09-AUG-2004  
 LOCUS AY378150  
 DEFINITION Phalaenopsis equestris MADS box transcription factor (MADS3) mRNA,  
 complete cds.  
 VERSION AY378150  
 ACCESSION AY378150.1 GI:36680586  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Phalaenopsis equestris  
 Phalaenopsis equestris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 Epidendroideae; higher Epidendroideae; Vandaeae; Aeridiinae;

## REFERENCE

1 (bases 1 to 980)  
 AUTHORS Tsai,W.C., Kuo,H.C.S., Chuang,M.H., Chen,W.H. and Chen,H.H.  
 TITLE Four DEF-Like MADS Box Genes Displayed Distinct Floral  
 JOURNAL Morphogenetic Roles in Phalaenopsis Orchid  
 PUBMED Plant Cell Physiol. 45 (7), 831-844 (2004)  
 15295066  
 REFERENCE 2 (bases 1 to 980)  
 AUTHORS Tsai,W.C., Chen,W.H. and Chen,H.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-SEP-2003) Department of Biology, National Cheng Kung  
 University, 1 University Rd., Tainan, Taiwan 701, Republic of China

## FEATURES

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## CDS

## ORIGIN

## Alignment Scores:

Prod. No.: 7,36e-61 Length: 980  
 Score: 758.50 Matches: 142  
 Percent Similarity: 81.94% Conservative: 44  
 Best Local Similarity: 62.56% Mismatches: 36  
 Query Match: 64.44% Indels: 5  
 Gaps: 2

US-10-690-246a-2 (1-227) x AY378150 (1-980)

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 DB 196 ATGGGCGGGGAAAGATCGAGATTAGAGATTCAGAACTCGACGAATCCGCGAGTCACT 255  
 QY 21 TyrSerIleValArgValAlaGlyIleLeuIleValSerIleValSerIleValSerIleValSer 40  
 DB 256 TACTTGAAGGAGGCGCTGAGATCATGAAAGCGGACGAGCTCAAGTCTCTGATGAT 315  
 QY 41 AlaGlnValSerIleValSerIleValSerIleValSerIleValSerIleValSerIleValSer 60  
 DB 316 GCTACGCTCTCCCTTGTATGTTCTCCAGCACCGGAGAGTTCGCCAGTATTGATGCT 375  
 QY 61 SerThrApilIleValSerIleValSerIleValSerIleValSerIleValSerIleValSerIleValSer 80  
 DB 376 ACCACCGATACCAAGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 435  
 QY 81 AsnAlaGlnValSerIleValSerIleValSerIleValSerIleValSerIleValSerIleValSer 100  
 DB 436 AGCAGACGATACGAGAGATGAGAAATACGTGTAATATTGAAAGATTAACACACACAC 495  
 QY 101 LeuArgIleValSerIleValSerIleValSerIleValSerIleValSerIleValSerIleValSer 120  
 DB 496 TTGAGAGGAGATTAAGCAGAGATGCGGAGAGATTTGAAGGCTTAAGAAATCAAGAA 555  
 QY 121 LeuArgIleValSerIleValSerIleValSerIleValSerIleValSerIleValSerIleValSer 140  
 DB 556 CTGCGGTGCTTGAAGAAATATGACAGAGCGCTTAAGCTGTGTAAGAAATCGAAAGTAT 615  
 QY 141 HisValIleAlaThrGlnThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 160

Db		616	CACGTCATCAGACACCACCGAATGATCACTTCCAAAAGTTGGAAAAACTCTCCAAAGAAC	675
Oy		161	TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluValProAsnTyrGlyPheAsn	180
Db		676	CACAGGAAGCTTAAGTCCGGAGACTG-----GAAACTGAGACGCAGCTTAACTAC	723
Oy		181	ValGluAsnGlnSerHisArgIleTyrGluAsnSerIleProMetValAsnGluCyPrroGln	200
Db		724	GTTGATGTATGATCCAAACACTGATGATGCCCGCTTGACCTGGAAATGGGGCTTCCCTAC	783
Oy		201	MetPheSerPheArgValValHisProAsnGlnProAsnLeuLeuGlyTyrGly	220
Db		784	TTGATTATTTATTTCT--ACCCACAACGACGACCGAAGCTTCAAGGAGTTGATATGTC	840
Oy		221	SerHisAspLeuSerLeuAla	227
Db		841	CCTCATGATCTTACGCTCGCC	861
RESULT 7				
AY378148		LOCUS	1030 bp mRNA linear	PLN 09-AUG-2004
DEFINITION			Phalaenopsis equestris MAD55 transcription factor (MAD5) mRNA,	
ACCESSION			Complete cds.	
VERSION			AY378148	
KEYWORDS			AY378148.1 GI:45935300	
SOURCE				
ORGANISM			Phalaenopsis equestris	
			Phalaenopsis equestris	
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
			Eurycoria; Viridiplantae; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;	
			Epipendroidae; higher Epipendroidae; Vandaea; Meridiinae;	
			Phalaenopsis.	
REFERENCE			1 (bases 1 to 1030)	
AUTHORS			Tsai,W.C., Khoo,C.S., Chuang,M.H., Chen,W.H. and Chen,H.H.	
TITLE			Four DEF-like MAD5 Box Genes Displayed Distinct Floral	
JOURNAL			Morphogenetic Roles in Phalaenopsis Orchid	
PUBMED			Plant Cell Physiol. 45 (7), 831-844 (2004)	
REFERENCES			15295066	
JOURNAL			2 (bases 1 to 1030)	
AUTHORS			Tsai,W.C., Chen,W.H. and Chen,H.H.	
TITLE			Direct Submission	
JOURNAL			Submitted (02-SEP-2003) Department of Biology, National Cheng Kung	
FEATURES			University, 1 University Rd., Tainan, Taiwan 701, Republic of China	
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			KEIKORKENLEGAVELRGLDEQLSESVIVQRKHVIATGYDCRRKLKSRRDI	
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			"D"	
ORIGIN				
Alignment Scores:				
Fred. No.:			1.64e-60	Length: 1030
Score:			755.00	Matches: 149
Percent Similarity:			82.59%	Conservative: 36
Best Local Similarity:			66.52%	Mismatches: 29
Query Match:			64.15%	Indels: 10
DB:			8	Gaps: 2

US-10-690-246A-2 (1-227) x AY378148 (1-1030)

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OY      1 MetGlyArgGlyLysIleGluIleLysLysIleGluAsnProThrAsnAlaGlnValThr 20
Db      255 ATGGGAGAGAGGAAAGATAGATTAAGAAATAGAGATCCAAACMACAGGCAAGTATGAC 314
OY      21 TyrSerLysAspGAGValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCysAsp 40
Db      315 TATTCAAAAGAGCGCACTTGGGATCATATAAAGGACAGAGAACTCACAGTGCCTCGGAC 374
OY      41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60
Db      375 GCTCAACTCTCATCATCATCTTCTTCAAGCTCCGGCAAGTTAGCTGATTTCTGCAGCCCT 434
OY      61 SerThrAspIleLysGlyIleTyrGluArgTyrGlnValAlaThrGlyMetAspLeuTyr 80
Db      435 TCCACAGACGGTTAAAGATATAGTTGAGAGAGGTACCAAAATGTTACCGGAATGTATATG 494
OY      81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsn 100
Db      495 GATCGCGAATTCACAGAGATGCGAACAACCTCTGAGGAATCTCAGGAGATTTAATCGTAT 554
OY      101 LeuArgLysGluIleArgArgArgLysGlyGluGluLeuLeuGluGluMetAspIleLysGln 120
Db      555 CTTCAAGAGAGGATATAGACACAGAGGAGGAGGAATCTGAAAGGGTGGCGCTTAAAGAG 614
OY      121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValAlaGlnHisArgLysTyr 140
Db      615 CTGGCGCGGTCTTGAGCAAAATTTGAGAGAGCTGGTAAAGATTGTTCCGACAGAGAAAGTAT 674
OY      141 HisValIleAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160
Db      675 CATGTGATCGCTACGCAAAACAGACACTTGACGAGAAAGCTCAAAAGCACACAGCAATA 724
OY      161 TyrArgAlaLeuIleHisGluLeuAsp---MetLysGluGluAsnProAsnTyrGlyPhe 179
Db      735 TACAGAGCGCCCTAAGCGCATGAACTGCACAAAGCTGGACCAAGATCAACCGTCGACGTTT 794
OY      180 AsnAlaGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysPro 199
Db      795 CTCGTAGAGAGTCTTAAGCTGCATTAAGACGCTCAATCTCAATGCCAAATTCG----- 848
OY      200 GlnMetPheSerPheArgValAlaHisProAsnGlnProAsnLeuGluLysGlyTyr 219
Db      849 -----CTGCACCGGAGGTGAGCCAAATGCGAAGAAATGATGCT 887
OY      220 GluSerHisAsp 223
Db      888 GAGTGTCTCATGAG 899

RESULT 8
AF209729      833 bp      mRNA      linear      PLN 01-DEC-2000
LOCUS      HemeroCallis hybrid cultivar putative MADS box transcription factor
DEFINITION      (MADS1) mRNA, complete cds.
ACCESSION      AF209729
VERSION      AF209729.1
KEYWORDS      GI:11494136
SOURCE      HemeroCallis hybrid cultivar (daylily)
ORGANISM      HemeroCallis hybrid cultivar
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Asparagales;
Hemerocallidaceae; HemeroCallis.
1 (bases 1 to 833)
Lange,N.E.
REFERENCE
AUTHORS      Lange,N.E., Valpuesta,V., Napoli,C.A., Labavitch,J.M. and Reid,M.S.
TITLE      Molecular changes during the expansion and senescence of
ethylene-insensitive daylily flowers
JOURNAL      Thesis (1999) University of California, Davis
AUTHORS      Lange,N.E., Valpuesta,V., Napoli,C.A., Labavitch,J.M. and Reid,M.S.
TITLE      Direct Submission
JOURNAL      Submitted (30-NOV-1999) Environmental Horticulture, University of

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FEATURES California, Davis, CA 95616-8587, USA  
Location/Qualifiers

1. .833 /organism="Hemerocallis hybrid cultivar"

/mol\_type="mRNA"

/cultivar="Cradle Song"

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RLA"

# ORIGIN

## Alignment Scores:

Pred. No.: 4.77e-59 Length: 833  
Score: 738.00 Matches: 144  
Percent Similarity: 78.85% Conservative: 35  
Best Local Similarity: 63.44% Mismatches: 42  
Query Match: 62.70% Indels: 6  
DB: Gaps: 3

US-10-690-246a-2 (1-227) x AF209729 (1-833)

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QY 21 TySerIysArgGValIleGluIleValSerIleGluIleValSerIleGluIleValSer 40
DB 61 TACTCAAGAGAGAGTCTGATCATGAAAGCAAGCAAGTCTGCTGCTGAT 120
QY 41 AlaGlnValSerIleIleMetPheSerSerThrGlyIleValSerIleGluIleValSer 60
DB 121 GGTGACGTGTCATCATCATGATCTCGAGCACCGGCAAGTCTCGAGTATTCGAGCC 180
QY 61 SerThrAspIleValSerIleGluIleValSerIleGluIleValSerIleGluIleVal 80
DB 181 GGCACCTGACAGCAAGAGTGTGTTGAGAGTATTCAGCAGCGCAGCAGACAACTTGTG 240
QY 81 AsnIleGlnIleValSerIleGluIleValSerIleGluIleValSerIleGluIleVal 100
DB 241 AGTACACATATGAGAAATGCAAAACATGATCATCTCAAGAGATCAACATAT 300
QY 101 LeuArgIleGluIleValSerIleGluIleValSerIleGluIleValSerIleGluIle 120
DB 301 TTGGCCAGCAAGAAATTAGGACAGAGATGGAAGCAACTTGATGCGATGATTTCAAGGA 360
QY 121 LeuArgIleGluIleValSerIleGluIleValSerIleGluIleValSerIleGluIle 140
DB 361 CTGCGCGGTCTTGACCAAAATCTGATGAGAGCTTTGAAAGAGTTCGCGCTAGGAAAT 420
QY 141 HisValIleAlaThrGlnThrAspThrIleValSerIleGluIleValSerIleGluIle 160
DB 421 CATGCGATTACCATCTGACGATGATCTCAAGAAAGAGTGAAGAATTTCCCAAGAGA 480
QY 161 TyrArgAlaLeuIleHisGluLeuAspMetIleGluIleValSerIleGluIleValSer 180
DB 481 CACAGACATTTGCTGACGAACTGAT-----GAGCAGATGATGATGATGATGCG 528
QY 181 ValGluAsnGlnSerArgIleIleValSerIleGluIleValSerIleGluIleValSer 200
DB 529 GATGAGGACCCAGGCAAC---TATGATGATGATGATGATGATGATGATGATGATGAT 585

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QY 201 MetPheSerPheArgValIleHisProAsnGlnProAsnLeuIleGluIleValSerIle 220  
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QY 221 SerHisAspLeuSerLeuAla 227  
DB 643 CCACATGATCTTCTGCTTGA 663

## RESULT 9

AB094965

LOCUS

DEFINITION

AB094965

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AB094965 1002 bp mRNA linear PLN 31-OCT-2003

Tulipa gesneriana TGDEFA mRNA for MADS-box transcription factor,

complete cds.

AB094965

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RESULT 11	1016 bp	mRNA	linear	PLN 31-OCT-2003
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LOCUS	1016 bp	mRNA	linear	PLN 31-OCT-2003
DEFINITION	Tulipa gesneriana TGDEB mRNA for MADS-box transcription factor,			
ACCESSION	AB094966			
VERSION	AB094966.1			
KEYWORDS	GI:30172222			
SOURCE	Tulipa gesneriana			
ORGANISM	Tulipa gesneriana			
REFERENCE	Bukartovic, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Tulipa.			
AUTHORS	Kanno, A., Saeeki, H., Kameya, T., Saedler, H. and Theissen, G.			
TITLE	Heretropic expression of class B floral homeotic genes supports a modified ABC model for tulip (Tulipa gesneriana)			
JOURNAL	Plant Mol. Biol. 52 (4), 831-841 (2003)			
MEDLINE	22856392			
PUBMED	13677470			
REFERENCE	2 (bases 1 to 1016)			
AUTHORS	Kanno, A.			
TITLE	Direct Submission			
JOURNAL	Submitted (28-OCT-2002) Akira Kanno, Tohoku University, Graduate School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi 980-8577, Japan (E-mail:kanno@life.tohoku.ac.jp, Tel:81-22-217-5725, Fax:81-22-217-5725)			
FEATURES	Location/Qualifiers			
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ORIGIN				
Alignment Scores:				
Pred. No.:	1.42e-55	Length:	1016	
Score:	701.50	Matches:	136	
Percent Similarity:	78.70%	Mismatches:	45	
Best Local Similarity:	59.13%	Indels:	5	
Query Match:	59.60%	Gaps:	3	
DB:	8			
US-10-690-246A-2 (1-227) x AB094966 (1-1016)				
Qy	1 MetGTAAGGGLyVellleGluilleVlyslleGluasProthrasnarGlnValThr 20			
Db	71 ATGGGCGCGGAGATTCAGATCAAGAAATTGAGACTCAACCAACGTCAGGTACT 130			
Qy	21 TYSerLYSARGArGValGlylleuLYslySaLaLyAGluLeuThrValleuCYaSP 40			
Db	131 TATTCCAAACGTCGTATGTGGGATCATGAAAGGCCAATGAATCACTGCTCTTGCGAC 190			
Qy	41 ALaGlnValSerleuIleuMetPheSerSerThrGlyLyLeuAlaAspYrCYsSerPro 60			
Db	191 GGTGAAGTTTCACTAATTATGTTTCAACACATCAAGAACCTCCCAAGTTTGGACATGAA 250			
Qy	61 SerThrAspRIleVagIlylleYrGluATGyrGlnValValThrGlyMetAspLeuTrp 80			

Db		251	TCCACCAATCAGAAAAAAGATCTTCGATCGGTACACAGCATGACTGGATCAACCTGTGG	310
Qy		81	AenAlIGlnTyrGIuaRwMcGInaBnThrLeuLysHisLeuAsnGluIleAsnGlnAsn	100
		::::	::::	::::
Db		311	AGGCCCAATACAGACAGAAATGCAGAATTACGTTCCMACCATCTGAGCCAGATCAACCGTAAC	370
Qy		101	LeuArgLyGIuIlleaRgArGlyVsgLYGIuLeuGluGluYmeArSpILeLysGln	120
		::::	::::	::::
Db		371	CTTCGCAAGGGAATAAAGCAGACAGATGGGGAGACAGCTGATGTCTTGACACGACAAG	430
Qy		121	LeuArgGLYeuGIuGlnThrLeuGIuSerLeuArgILEValaRghIsarGlyeTYr	140
		::::	::::	::::
Db		431	CTCCGGGCTTACGCAAAATTTGGAGCGCGCTTGAAGCTTGTCTGTGGAGAAAGTAT	490
Qy		141	HISValIlealathrglnthrAspHTrTYrLYelyleLeuLysSerThrArGluThr	160
		::::	::::	::::
Db		491	CATGTCCTTGATCTCAGATAGAAAACCTTCMAAAAAAGGTGAAAAATTACGGGGAACCT	550
Qy		161	TYrARgAlaleuIleHisGLueU-----ASPmetLySGluGlnAsnProAsnTYr	177
		::::	::::	::::
Db		551	AATAACAACCTTACTCCGCGACCTGTGGACATAGATGAATAATAGCACCATGTATT	610
Qy		178	GLYpheanArgIuAnGlnSerArGILeTYrGIuAsnSerIlePrometValAsnGlu	197
		::::	::::	::::
Db		611	GGTATT--GTGATGATTAACCCGACACAGCTATGAGGTGGCTGTGCTGGCTAAATGGG	667
Qy		198	CysProGlnMetPheSerPheaRGValaIleHieProAsnGlnProAsnLeuLeuGlyeu	217
		::::	::::	::::
Db		668	GGGTCTAGCATGTATGACAGATTCCCG--ATCCAACCTTAGCAGCAACCTCATGTATG	724
Qy		218	GLYTyrGIuSerHisapLeuSerLeuLA	227
		::::	::::	::::
Db		725	GGTACCGACTACATGATCTTTGTCTGTCT	754
RESULT_12				
AF230706		938 bp	mRNA	linear
LOCUS				PLN 02-JUN-2000
DEFINITION			Tacca chantieri MADS box transcription factor AP3 mRNA, partial	
ACCESSION		AF230706		
VERSION		AF230706.1	GI:8163953	
KEYWORDS				
SOURCE				
ORGANISM				
			Tacca chantieri	
			Tacca chantieri	
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
			Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales;	
			Dioscoreaceae; Tacca.	
REFERENCE			1 (bases 1 to 938)	
AUTHORS			Kramer,B.M. and Irish,V.F.	
TITLE			Evolution of the petal and stamen developmental programs: Evidence	
JOURNAL			from comparative studies of the lower eudicots and basal	
			angiosperms	
			Int. J. Plant Sci. (2000) In press	
FEATURES				
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			/FTIDLSQSIFERKQNNLNHLIEINRLREIRFORPTGEDIDGDIDIELRLGEON	
			RYYQVTGLIVRRKHVVITDTDTYTKKLKNSHEARNLRLEIKEMDEHFVIYGFVNDPDP	
			VNDSALMLVANGSHVAVRYVPSPNPJHGIGYSHDRLA"	
CDS				

## ORIGIN

## Alignment Scores:

Pred. No.: 1.78e-55 Length: 938  
 Score: 700.00 Matches: 130  
 Percent Similarity: 84.08% Conservative: 39  
 Best Local Similarity: 64.68% Mismatches: 30  
 Query Match: 59.47% Indels: 2  
 DB: 8 Gaps: 2

US-10-690-246a-2 (1-227) x AF230706 (1-938)

QY 27 GlyIleuLysAlaValSerLeuThrValLeuCyAspAlaGlnValSerLeu 46  
 Db 4 GGGATCATGAAGAAGCCAGAGAGCTCAAGCTCTTGGCATGCTAGGTTCTATCATC 63  
 QY 47 MetPheSerSerThrGlyLysLeuAlaAspTyrCysSerProSerThrAspIleLysGly 66  
 Db 64 ATGTTCTCCAGCACTGGCAAGTTCCGCCAGTACAGTCCCTTCCACCGATACGAAGAG 123  
 QY 67 IleTyrGluArgTyrGlnValValThrGlyMetAspLeuThrAsnAlaGlnTyrGluArg 86  
 Db 124 GTTATGATCGGATCCGACCAAGTGAAGTGGATGACCTGTGGAGTTCGACGAGAGG 183  
 QY 87 MetGlnAsnThrLeuLysIleLeuAsnGluIleAsnGlnAsnLeuArgLysGluIleArg 106  
 Db 184 ATGCAGAAATAACTGATCATCTGGAGAGATCAACCGAATCTTCGAGAGGAATTAAG 243  
 QY 107 ArgArgLysGlyGluGluLeuGluGlyMetAspIleLysGlnLeuArgGlyLeuGluGln 126  
 Db 244 CAAGGACGCGGCGAAGATCTTGACGGCTTGACATCAAAAGCTGCTGTGGAGCA 303  
 QY 127 ThrLeuGluLysSerLeuArgIleValArgHisArgLysTyrHisValIleAlaThrGln 146  
 Db 304 AATGTGATGAGCTTTGAGGATTTGTCGTCAAAGGAATATCATGTTATCACACACAG 363  
 QY 147 ThrAspThrTyrLysLysLysLeuLysSerThrArgGluThrTyrArgAlaLeuIleHis 166  
 Db 364 ACCGATATCATATAAAGAGAGCTGAAGAATTCCTCCATGAAGCTCAAGAGAACTATGCGA 423  
 QY 167 GluLeuAspMetLysGluGluAsnProAsnTyrGlyPheAsnValGluAsnGlnSerArg 186  
 Db 424 GAACCTGAGATGAGAGATGAGACCCAGTTTACGGGGTTC---GTCCAGATGATCTTACT 480  
 QY 187 IleTyrGluAsnSerIlePheMetValAsnGluCysProGlnMetPheSerPheArgVal 206  
 Db 481 AACTACGACAGCGCTGTGGCATGGCAATGCTGGGTCTCATGTCTACGGGTACCGT--- 537  
 QY 207 ValHisProAsnGlnProAsnLeuLeuGlyLysGlyTyrGluSerHisAspLeuSerLeu 226  
 Db 538 GTTCAGCGCAAGCCAGCAATCTCCATGGAATAGGGCTTCTCATGACCTTCGCGCTG 597  
 QY 227 Ala 227  
 Db 598 GCA 600  
 RESULT 13  
 AB003323 1084 bp mRNA linear PLN 21-MAR-2002  
 LOCUS  
 DEFINITION  
 Oryza sativa (japonica cultivar-group) mRNA for MADS box-1 like  
 protein, complete cds, clone:E20969.  
 ACCESSION  
 AB003323  
 VERSION  
 AB003323.1 GI:5295979  
 SOURCE  
 MADS box-1 like protein.  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Rharioideae; Oryzaceae; Oryza.  
 REFERENCE  
 1 Shinozuka, Y., Yamamoto, K. and Sasaki, T.  
 AUTHORS  
 TITLE  
 Characterization of rice MADS box-1 like genes  
 JOURNAL  
 Unpublished

## REFERENCE 2 (bases 1 to 1084)

AUTHORS  
 TITLE  
 JOURNAL  
 Submitted (23-APR-1997) Takuji Sasaki, National Institute of  
 Agricultural Resources, Rice Genome Research Program, Kamondai  
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
 (E-mail: tsasaki@agr.affrc.go.jp, Tel:0298-38-7441,  
 Fax:0298-38-7468)  
 FEATURES  
 Location/Qualifiers  
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 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:39947"  
 /clone="E20969"  
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 /product="MADS box-1 like protein"  
 /product\_start=1  
 /product\_end=1084  
 /protein\_id="BA081881.1"  
 /db\_xref="GI:5295980"  
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 IIMFSTGKYHEFCSPSTDIKGIFDRYQDALGSLIMIQYENMORTLSHLDINLR  
 TIRORMGEDLDGLFDELRGLQVNDALKEVRRKHYVITQTEYKKVKSUYEA  
 YETLOOELGLREBPAPFGFVDNTGGWDGAGAAADMPAFRVVPSQPLHGMAYGN  
 HILRLG"

## CDS

Alignment Scores:  
 Pred. No.: 5.69e-54 Length: 1084  
 Score: 684.50 Matches: 138  
 Percent Similarity: 75.77% Conservative: 34  
 Best Local Similarity: 60.79% Mismatches: 50  
 Query Match: 58.16% Indels: 5  
 DB: 8 Gaps: 5

## ORIGIN

US-10-690-246a-2 (1-227) x AB003323 (1-1084)

QY 1 MetGlyArgGlyLysIleGluLysLysIleGluAsnProThrAsnArgGlnValThr 20  
 Db 102 ATGGGAGAGGGGCAAGATTCAGATCAAGCGGATCGAGAACGCAACAGGAGGTGACC 161  
 QY 21 TyrSerLysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCyAsp 40  
 Db 162 TACTCGAAGCGCGCAGCGGATCATGAAGAAGCCAGGAGACTCACTGCTTCGAC 221  
 QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60  
 Db 222 GCCCAGGTGGCATCATGATTTCTTCCTCCACGGCAAGTACACGAGTTTCGACGCT 281  
 QY 61 SerThrAspIleLysGlyLysTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp 80  
 Db 282 TCCACCGACATCAAGGGGATCTTTGACGCTACAGCAAGCCATCGGACCAAGCTTTGG 341  
 QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysIleLeuAsnGluIleAsnGlnAsn 100  
 Db 342 ATCGAGCAATATGAATATGACGCGCAGCTGAGCACTTCAAGACATCAACCGCAAC 401  
 QY 101 LeuArgLysGluIleArgArgArgLysGlyGluGluLeuGluGlyMetAspIleLysGln 120  
 Db 402 CTGCGCAGCAGATCGAGCAAGAGATGGGAGAAGATCTGAGACGGGCTGAGTTCCAGAG 461  
 QY 121 LeuArgLysGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140  
 Db 462 CTGGCGGCTTGAAGAAATATGATGCGGCTTCAGAGAGTTTCGACAGGAAGTAT 521  
 QY 141 HisValIleAlaThrGlnThrAspThrTyrLysLysLeuLysSerThrArgGluThr 160  
 Db 522 CATGTATCAACCAAGACTGAACCTTCAAGAAAGGTGAAGACTCTTCAAGAGGG 581  
 QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrGlyPheAsn 180



Db	582	TACGAGACTTCGACGACGACCTGGGCTTCGGGAGAG---CCGGCGTTCGGGCTTC---635
Qy	181	ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCyProGln200 
Db	636	GTCGACACACACCGGCGCGGGTGGACGCGGCGCGCGC---GCCGGCGGCGCGCGAC692 
Qy	201	MetPheSerPheArgValValHisProAsnGlnProAsnLeuLeuGluGlyTyr---219 
Db	693	ATGTTCGCCCTTCGCGCGGTGG---CCGACGCCACGCCCACTGCACGCGCATGGCTACGCG749 
Qy	220	GluSerHisAspLeuSerLeu226 
Db	750	GGCAACACGACGACCTGGCGCTTC770 
RESULT 14		
AK069317		
LOCUS	AK069317	1210 bp mRNA linear PLN 24-JUL-2003
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone:J023014M24, full insert sequence.	
ACCESSION	AK069317	GI:32979341
VERSION	AK069317.1	FLI CDM: CAP trapper.
KEYWORDS	Oryza sativa (japonica cultivar-group)	
SOURCE	Oryza sativa (japonica cultivar-group)	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.	
REFERENCE	1 The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Ohtomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Kobayashi, S., Nishikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN: Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Oota, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.	
AUTHORS	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice Science 301 (5631), 376-379 (2003)	
JOURNAL	2 (bases 1 to 1210)	
MEDLINE	12869764	
REFERENCE	22752273	
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nishikura, J., Nishikura, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Oota, N., Ota, Y., Ohtomo, Y., Ryu, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.	
TITLE	Direct Submission	

JOURNAL	Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skkuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)	
COMMENT	This clone is one of the 28K full-length cDNA clones from japonica rice. URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.	
	FAIS Genome Sequencing & Analysis Group: Ohtomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nishikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.	
	Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.	
FEATURES	location/Qualifiers	
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ORIGIN		
Alignment Scores:	6.46e-54	Length: 1210
Pred. No.:	684.50	Matches: 138
Score:	75.77%	Conservative: 34
Percent Similarity:	60.79%	Mismatches: 50
Best local Similarity:	58.16%	Indels: 5
Query Match:	8	Gaps: 5
DB:	US-10-690-246A-2 (1-227) x AK069317 (1-1210)	
Qy	1	MetGlyArgGlyIleValIleGluIleValIleGluAsnProThrAsnArgIleValThr20
Db	216	ATGGGAGGGGCGAAGATCGATCAACGGATGAGAACCCGACCAACAGCGATACCC275
Qy	21	TyrSerIysArgArgValGlyIleLeuValAlaIleValGluLeuThrValLeuCyAsp40
Db	276	TACTCGAAGGCGCGACGGGATCATGAAGAAGCCAGGAGCTCACGTAATCTCGAC335
Qy	41	AlaGlnValSerLeuIleMetPheSerSerThrGlyIleValLeuAlaAspTyrCySerPro60
Db	336	GCCCAAGTCCCATCAATCAATGTTCTCTCCACCGGCAAGACCAACGAGTTCTGAGCCT395
Qy	61	SerThrAspIleIleGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr80
Db	396	TCCACCAACATCAAGGGGAACTTTGACCGCTACCAACACCATCGCACCAGCTTTGG455
Qy	81	AsnAlaGlnTyrGluArgMetGlnAsnThrLeuValIleLeuAsnGluIleAsnGlnAsn100
Db	456	ATGAGCAGATATGAGATATGACAGCGCATGTCATCAAGACATCAACCGCAAC515
Qy	101	LeuArgIleGluIleArgArgArgIleGlyIleGluIleLeuGluIleGluMetAspIleLeuGln120



GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus.p2n model

Run on: October 6, 2005, 10:27:46 ; Search time 558 Seconds  
(without alignments)  
2408.210 Million cell updates/sec

Title: US-10-690-246A-2

Perfect score: 1177  
Sequence: 1 MRRGKRIEIKIENPTNRQYT.....HPNQPLVLGIYSHSLSLA 227

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 segs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:  
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-O=Cpnt2\_1/USPTO.apool/US10690246/runat 05102005 110909 6425/app.query.fasta\_1.391  
-DB=N\_genseq\_16Dec04 -OPMT=fastacp -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPTCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=dl0sum62 -TRANS=human40.cdt  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MTN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USR=US10690246 @CGN 1.1 470 @runat 05102005 110909 6425 -NCPU=6 -ICPU=3  
-NO MAMP -IARGODIRY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEF\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Genseq\_16Dec04:\*

1: genseq11980s:\*\n2: genseq11990s:\*\n3: genseq12000s:\*\n4: genseq12001as:\*\n5: genseq12001bs:\*\n6: genseq12002as:\*\n7: genseq12002bs:\*\n8: genseq12003as:\*\n9: genseq12003bs:\*\n10: genseq12003cs:\*\n11: genseq12003ds:\*\n12: genseq12004as:\*\n13: genseq12004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	57.3	681	12	ADJ44530 Plant CDN
2	675	57.3	1257	6	AAD42257 Corn AP3
3	675	57.3	1257	13	ADRD4278 Corn AP3
4	611	51.9	681	4	AAF85393 Nucleicid
5	611	51.9	946	4	AAF85392 Nucleicid

6	611	51.9	946	6	ABR88485
7	611	51.9	946	9	ACA62518
8	595	50.6	924	3	AA57943
9	576	48.9	637	10	ADK59650
10	557.5	47.4	926	6	ADJ42259
11	557.5	47.4	926	13	ADRD4282
12	528.5	44.9	644	13	ACN53850
13	528	44.9	882	2	AAQ51189
14	526.5	44.7	982	4	AA500104
15	521.5	44.3	630	10	ADK59791
16	509.5	43.3	664	10	ADK56100
17	509.5	43.3	665	10	ADK59635
18	509.5	43.3	954	3	AA51525
19	509.5	43.3	988	12	ADQ61550
20	509.5	43.3	1170	3	AA51790
21	507.5	43.1	959	3	AA40831
22	486	42.1	989	3	AA55879
23	485	41.2	954	3	AA40685
24	480	40.8	498	12	ADP95468
25	432	36.7	951	13	ADRD61340
26	427.5	36.3	639	13	ACN53901
27	415.5	35.3	868	4	AA500103
28	414	35.2	425	12	ADQ03168
29	413	35.1	649	13	ACN54118
30	412	35.0	407	12	ADQ06448
31	406	34.5	601	13	ACN58761
32	400	34.0	896	10	ADK55880
33	400	34.0	914	12	ADQ01642
34	400	34.0	914	12	ADQ01652
35	400	34.0	947	3	AA539436
36	399	33.9	632	10	ADK55993
37	397	33.7	742	10	ADK56091
38	393	33.4	474	12	ADP95656
39	391.5	33.3	674	10	ADK56104
40	386	32.8	401	12	ADQ03167
41	385	32.8	780	2	AAQ503170
42	385	32.7	780	2	AAQ503170
43	382.5	32.5	535	12	ADP94271
44	378	32.1	909	3	AA535208
45	371.5	31.6	1089	6	AAJ42258

## ALIGNMENTS

RESULT 1	
ADJ44530	standard; cDNA; 681 BP.
ID	ADJ44530;
AC	ADJ44530;
DT	06-MAY-2004 (first entry)
DB	Plant cDNA #5530.
XX	Plant; gene; ss; transcription; plant genome augmentation; cereal;
XX	soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
XX	malt; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
XX	stress tolerance; salt tolerance; cold tolerance; dwarfism; early flowering; antiviral;
XX	antifungal.
OS	Eukaryota.
XX	US2004016025-A1.
XX	22-JAN-2004.
XX	26-SEP-2002; 2002US-00260238.
XX	26-SEP-2001; 2001US-0325277P.
XX	26-SEP-2001; 2001US-0325448P.
XX	04-APR-2002; 2002US-0370620P.

ABK88485	Poplar pr
ACA62518	Poplar ho
AA57943	Poplar fl
ADK59650	Plant DNA
ADJ42259	Soybean A
ADRD4282	Soybean A
ACN53850	Cotton an
AAQ51189	Homeotic
AA500104	Granny Sm
ADK59791	Plant DNA
ADK56100	Plant DNA
ADK59635	Plant DNA
AA51525	Arabidops
ADQ61550	Transcrip
AA51790	Arabidops
AA40831	Arabidops
AA55879	Eucalyptu
AA40685	Arabidops
ADP95468	Cotton ex
ADRD61340	Cotton cd
ACN53901	Cotton an
AA500103	Granny Sm
ADQ03168	Arabidops
ACN54118	Cotton an
ADQ06448	Soybean t
ACN58761	Cotton gy
ADK55880	Thalecres
ADQ01642	Thalecres
ADQ01652	Transcrip
AA539436	Arabidops
ADK55993	Plant DNA
ADK56091	Plant DNA
ADP95656	Cotton ex
ADK56104	Plant DNA
ADQ03167	Arabidops
AAQ503170	Arabidops
AA55089	fbp1 cDNA
ADP94271	Cotton ex
AA535208	Arabidops
AAJ42258	Corn AP3





CC present invention.

**Sequence** 1257 BP; 320 A; 353 C; 340 G; 244 T; 0 U; 0 Other;

### Alignment Scores:

Pred. No.:	1,73e-62	Length:	125
Score:	675.00	Matches:	135
Percent Similarity:	75.14	Conservative:	37
Best local Similarity:	58.954	Mismatches:	51
Query Match:	57.354	Indels:	6
DB:	13	Gaps:	5

US-10-690-246A-2 (1-227) X ADR04278 (1-1257)

QY	1	MetGlyAARGGLyLyletIleGluIleLysLysIleGluAsnProThrAsnArgIleValThr	20
Db	131	ATGGGGCCGGCGAAGATTCAGAGTCAAGCCGAGTTCAGAAAGCCCAACCGCCAGGTGAC	130
QY	21	TySerIleYARGArgValGlyIleLeuLysLysAlaLysGluIleThrValLeuCyAsp	40
Db	131	TACTCCAAAGCCGCGACGGGGATCATGAAAGAGCGCGAGCTCAACCGTCTCGAC	250
QY	41	AlaGlnValSerIleuLeuMetPheSerSerThrGlyLysLeuAlaMetTyrcysSerPro	60
Db	251	GCCCAAGTCCGATCATCATGTTCTCTCCACCGGCAAGTACCAACAGATCTTCACACCC	310
QY	61	SerThrAspIleLysGlyLyleTyrguArgTyrglnValValThrGlyMetAspLeuTrp	80
Db	311	GGAAACGACATCAAGACCATCTTTAGCCGGTACACAGGCCATCGGGACACCACTATGG	370
QY	81	AsnAlaGlnTyrglyLysArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsn	100
Db	371	ATCGAGCACTATGAGAAATATGACGCCACGCGTGCATCTCAAGACATCAATCTGTGT	430
QY	101	LeuArgLysGluIleLeuArgArgTyrglyGlyGluIleuGluIleuLysMetAspIleLysGln	120
Db	431	CTGGCGACAGAGTTTATGGCAAGAGATGGCGAGAGATCTGGACAGTCTGGACTTCAGAG	490
QY	121	LeuArgGlyLeuGluGluIleThrLeuGluGluIleuSerLeuArgIleValAlaArgHisArgLysTy	140
Db	491	CTGGCGGGCTCGAGCAAAACGTGCACGCGGCTCTCAAGAGAGTTGGCCATAGAAAGTAC	550
QY	141	HisValIleAlaThrIleThrAspThrTyrglyLysLysLysLysSerThrArgGluThr	160
Db	551	CATGTGATAGACCGGACCTGATACTCTCAAAAAAGGTGAAGCACTGCACAGAGCG	610
QY	161	TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrglyPheAsn	180
Db	611	TACAAAGAACCTGACAGAGAGCTTAGGCAATGCGGAGGAC---CCGGGTTTCGGGTAC---	664
QY	181	ValGluAsnGlnSerArg-----IleTyrgluAsnSerIleProMetValAsnGluCys	198
Db	665	GTCGACCAACACCGGCGCCGCGCTGCGCTGGGACCGGCGCGCGCGCGCGCGCGCC	724
QY	199	---ProGlnMetPheSerPheArgValAlaHisProAsnGlnProAsnLeuLeuGlyLeu	217
Db	725	CCGCGGACATGTACCCCTTCCCGGTGGT---CCAGCCAGCCCAACCTGCACGGCATG	781
QY	218	GlyTyrgluSerHisAspLeuSerIleu	226
Db	782	GCCTACGGCTTCACGACCTCCGCCGTG	808
RESULT 4			
AAAF85393			
ID AAF85393 standard, cDNA, 681 BP.			
XX AAF85393;			
XX DT 23-JUL-2001 (first entry)			
XX Nucleotide sequence of the floral homeotic protein PTD.			
XX DE Floral homeotic gene; PTD; PTLF; PTAAG-1; PTAAG-2; floral tissue; LEAFY;			
XX KW			

## RESULT 4

ID AAF85393 standard; cDNA; 681 BP.

AC AAF85393

DT 23-JUL-2001 (first entry)

DE Nucleotide sequence of the floral homeotic protein PTD.

Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;

KM LRF; FLORICULTURA; FLO; DEICIENTS; DEF; AGAUS; AG; trasgenic plant,  
 KM fertility; sterility; ss.  
 XX  
 OS *Populus balsamifera*.

	Key	Location/Qualifiers
FA	CDS	1..681
FT		/*tag= a
FT		/product= "PTD"
FT		

PN CA2319853-A1.

PD 01-APR-2001.

PF 02-OCT-2000; 2000CA-02319853.

PR 01-OCT-1999; 99US-00410464.

PA (UYOR-) UNIV OREGON HEALTH SCI.  
XX  
XX

PI Rottman WH, Straubs SH, Brunner AM, Sheppard LA;  
XX

DR WP1; 2001-336098/36 -  
P-PSDB: AAB68435.  
DR

Novel isolated po

PT producing transgenic plants having particularly sterility.

PS Claim 25; Page 42-43; 69pp; English.

CC The present sequence encodes a floral homeotic protein, designated *PTD*.  
CC It is derived from *Populus balsamifera* subsp. *trichocarpa*. The  
CC specification also describes *PR1F*, *PTAG-1* and *PTAG-2* proteins. The floral  
CC homeotic proteins are expressed in floral tissues. *PR1F* is a homologue of  
CC *LEAFY* and *FLORICANTULA* (*FLO*), and is expressed in immature  
CC inflorescences on which floral primordia are developing. *PTD* is a  
CC homologue of *DEFICIENS* (*DBF*), and is strongly expressed in stamen  
CC primordia from the onset of organogenesis. *PTAG-1* and *PTAG-2* are  
CC homologues of *AGAMOUS* (*AG*). The floral homeotic proteins and  
CC polynucleotides are useful for producing transgenic plants having  
CC modified fertility characteristics, particularly sterility

Sequence 681 BP; 228 A; 148 C; 157 G; 148 T; 0 U; 0 Other;

**Alignment Scores:**

Pred. No.:	5,68e-56	Length:	681
Score:	611.00	Matches:	122
Percent Similarity:	70.69%	Conservative:	36
Best Local Similarity:	55.17%	Mismatches:	56
Query Match:	51.91%	Indels:	12
DB:	4	Gaps:	4

US-10-690-246A-2 (1-227) x AAF85393 (1-681)

[illegible]



ID ABK88485 standard; cDNA; 946 BP.  
 AC ABK88485;  
 DT 29-AUG-2003 (revised)  
 DT 07-OCT-2002 (first entry)  
 DE Poplar protein transduction domain, PTD, cDNA.  
 XX Poplar; ss; gene; plant; DEFICIENS; transgenic; promoter;  
 KM protein transduction domain; floral homeotic gene;  
 KM floral-specific expression; cytotoxin; fertility; sterility; PTLF;  
 KM PTA6-1; PTA6-2.  
 XX Populus balsamifera; subsp. trichocarpa.  
 OS  
 FH Key Location/Qualifiers  
 FT 1..684  
 FT /\*tag= a  
 FT /product= "PTD"  
 XX  
 PN US6395892-B1.  
 PD 28-MAY-2002.  
 PD 01-OCT-1999; 99US-00410464.  
 PF 06-APR-1998; 98US-0080861P.  
 PR 06-APR-1999; 99US-00287700.  
 XX  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 XX  
 PI Strauss SH, Rottmann W, Brunner A, Sheppard L;  
 DR WPI; 2002-572853/61.  
 DR P-PSDB; ABG30865.  
 XX  
 PT New protein transduction domain promoter nucleic acid molecule useful for  
 PT producing transgenic plants having modified fertility characteristics,  
 PT particularly sterility.  
 XX  
 XX Example 1; Col 35-38; 46pp; English.  
 PS  
 XX The invention relates to an isolated nucleic acid molecule especially a  
 CC protein transduction domain (PTD) promoter: (i) that hybridizes under  
 CC wash conditions of 0.2 x SSC (sodium citrate), 0.1 %SDS (sodium  
 CC dodecyl sulphate) at 65 plusoc to nucleotides or (ii) comprising 35  
 CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene  
 CC and is the homologue of DEFICIENS. Also includes are a recombinant  
 CC nucleic acid comprising the PTD promoter, a cell transformed with the  
 CC recombinant nucleic acid and a transgenic plant comprising the  
 CC transformed cell. The PTD promoter is useful to obtain floral-specific  
 CC expression of genes such as cytotoxins, that are employed in genetic  
 CC ablation strategies to produce trees having modified fertility  
 CC characteristics, including sterility. Genetic constructs comprising in  
 CC antisense versions or dominant negative mutants of PTD are useful in  
 CC producing genetically engineered Poplars and other trees, and for sense  
 CC suppression. Also disclosed are 3 other homeotic genes PTLF, PTA6-1 and  
 CC PTA6-2 (none are defined). The present sequence is the PTD cDNA. (Updated  
 CC on 29-AUG-2003 to standardise OS field)  
 XX  
 SQ Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.68e-56 Length: 946  
 Score: 611.00 Matches: 128  
 Percent Similarity: 70.69% Conservative: 36  
 Best Local Similarity: 55.17% Mismatches: 56  
 Query Match: 51.91% Indels: 12  
 DB: 6 Gaps: 4  
 US-10-690-246a-2 (1-227) x ABK88485 (1-946)

QY 1 MetGlyArgGlyLysLeuIleGluIleLysLysIleGluAsnProThrAsnArgIleValThr 20  
 DB 1 ATGGGTCTGTGAAAGATTGAAATTCAGAAAGATCGAAACCCCAAGAGCAAGTCAAC 60  
 QY 21 TyrSerLysArgArgValGlyIleLeuLysLysValLysGluLeuThrValLeuCySer 40  
 DB 61 TACTCGAAGAGAAAGAAATGTAATTTTCAGAAAGCCCAAGAACTCACTACTTGTGAT 120  
 QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60  
 DB 121 GCTAAGGTCTCTTATTCATGTTCTCCACACTTAACAACTGAATGATGATTAAGCCCC 180  
 QY 61 SerThrAspIleLysGlyIleTyrGluArgGlyGlnValValThrGlyMetAspLeuTrp 80  
 DB 181 TCCACATCGACAAAGAAAGATCTACGATCAATTCAGAAAGCTTTAGGCTAGATCTGTGG 240  
 QY 81 AsnAlaGlnTyrGluArgMetGluAsnThrLeuLysLysLeuAsnGluIleAsnGlnAsn 100  
 DB 241 GGCACCTCAATACGAGAAATTCAGAGACAGCACTGAGGAGACCTGAATGATCTAGATCA 300  
 QY 101 LeuArgLysGluIleArgArgArgLysGlyGluGluLeuGluGlyMetAspIleLysGln 120  
 DB 301 CTGAGACAAAGAAATTCAGGACAGAGAGAGAGGCGCTTAATGATCTAGATCTATCAT 360  
 QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140  
 DB 361 CTGCGCGGTCTTGAGAACATATGACTGAAGCTTGAATGTGTGGTGGCAGAAATGAC 420  
 QY 141 HisValIleAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160  
 DB 421 CATGTGATCAAAACAAACAAACAAACCTACAGAAAGAGTAAAGATTAGAGAGAGAGA 480  
 QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrGlyPheAsn 180  
 DB 481 CATGAAACCTCTTGATGGAATATGAGCAAAACTAGAGATCGACAGATAGTGTTA--- 537  
 QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200  
 DB 538 GTGGACAAAT-----GAAAGTGTGTTGCACTTGCAAAATGGGCTTCCAAAC 582  
 QY 201 MetPheSerPheArgValValHisProAsnGln-----ProAsnLeu--- 214  
 DB 583 CTCTATGCAATTCGCTGCATCAGGGCAACAACCAACCAACCAACCACTCTCTAATCTTCAAC 642  
 QY 215 LeuGlyLeuGlyTyrGluSerHisAspLeuSerLeu 226  
 DB 643 CTGGAGATGATTTTGAGCCCATGAACTTCGCTT 678  
 RESULT 7  
 ID ACA62518 standard; cDNA; 946 BP.  
 AC ACA62518;  
 DT 18-AUG-2003 (first entry)  
 DE Poplar homeotic gene PTD, cDNA.  
 XX Poplar; ss; gene; PTD; deficiens; homeotic gene; floral development;  
 KM sterile tree; pulp; paper; plant.  
 XX  
 OS Populus balsamifera subsp. trichocarpa.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..684  
 FT /\*tag= a  
 FT /product= "PTD"  
 FT /note= "This CDS is specifically claimed in claim 1"  
 XX  
 PN US2003033628-A1.  
 PD 13-FEB-2003.  
 XX



PF 21-MAR-2002; 2002US-00104580.  
 XX 06-APR-1998; 98US-0080851P.  
 PR 06-APR-1999; 99US-00287700.  
 PR 01-OCT-1999; 99US-00410464.  
 XX (UYOR-) UNIV OREGON HEALTH SCI.  
 XX Straus SH, Rottmann W, Brunner A, Sheppard L;  
 PI WPI; 2003-466273/44.  
 DR P-PSDB; ABU61893.  
 XX  
 PT New floral homeotic nucleic acid molecules, useful for the manipulation  
 of flowering in Poplar and other plant species, and for producing  
 PT transgenic plants having modified fertility characteristics, particularly  
 PT sterility.  
 XX  
 PS Claim 1; Page 20-21; 48pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule comprising at  
 CC least 15 consecutive nucleotides of the gene, cDNA or coding sequence of  
 CC 4 homeotic genes from poplar, PTF (LEAFY and FLORICA homologue), PTD  
 CC (DEFICIENS homologue), and PRAG-1/PRAG-2 (both homologues of AGAMOUS).  
 CC Also included are a recombinant nucleic acid molecule comprising a  
 CC promoter sequence operably linked to the nucleic acid molecule, a cell  
 CC transformed with the nucleic acid molecule, a transgenic plant comprising  
 CC the recombinant nucleic acid molecule and the purified proteins encoded  
 CC by the nucleic acids. The nucleic acid molecules are useful for the  
 CC manipulation of flowering in Poplar and other plant species, for  
 CC producing transgenic plants having modified fertility characteristics  
 CC (particularly sterility) and in the pulp and paper industries. The  
 CC present sequence is the poplar PTD cDNA  
 XX  
 XX Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8,68e-56 Length: 946  
 Score: 611.00 Matches: 128  
 Percent Similarity: 70.69% Conservative: 36  
 Best Local Similarity: 55.17% Mismatches: 56  
 Query Match: 51.91% Indels: 12  
 DB: 9 Gaps: 4  
 US-10-690-246a-2 (1-227) x ACA62518 (1-946)  
 QY 1 MetGlyArgGlyLysIleGluIleLysValIleGluAsnProThrAsnArgGlnValThr 20  
 DB 1 ATGGGTGTGTAAGATTTGAATCAAGAAATCGAAATCCCAACAAAGGCAAGTCAAC 60  
 QY 21 TySerIysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCysAsp 40  
 DB 61 TACTCGAAGAGAAAGAAATGATATTTCAGAAAGCCCAAGAACTCAGTCTTGTCAT 120  
 QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60  
 DB 121 GCTAAGGTCTCTTATCATATGTTCTCCAACTAAACAACTCAATGATCATTTAGCCCC 180  
 QY 61 SerThrAspIleLysGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp 80  
 DB 181 TTCACATCGACAAAGAAAGATCTACGATCATATTCAGAAAGCCTTTAGGCAATGATCTGG 240  
 QY 81 AsnIleGlnTyrGluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsn 100  
 DB 241 GGCACTCAATCGAAGAAATGCAAGAGACCTTGAGGAAGCTGAATGATATCATATCAAG 300  
 QY 101 LeuArgLysGluIleArgArgArgLysGlyGluGluLeuGluGlyMetAspIleLysGln 120  
 DB 301 CTGAGACAAAGAAATCGACGAGAGAGAGAGGCCCTGAATGATCTAGCACTTGATCAT 360  
 QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140  
 DB 361 CTGGCGGCTGTGAGCAACATATGACTAGAGCCTTGAATGGTGTGCTGGCAGGAATGAC 420

QY 141 HisValIleAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160  
 DB 421 CATGTATCAAAAACACAAAACGAAACCTTCAGAGAAAGGTGAAGAAATTTAAGAGAGAGA 480  
 QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrGlyPheAsn 180  
 DB 481 CATGAAACCTCTTATGATGAAATATGAAGCAAAACTAGAGATCGACATATGGTTTAA--- 537  
 QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200  
 DB 538 GTGACCAAT-----GAACTGCTGTTCACCTTGCAATGGAGGCTTCAC 582  
 QY 201 MetPheSerPheArgValValHisProAsnGln-----ProAsnLeu--- 214  
 DB 583 CTTATGACATTCGCTGATCAGCGGCAACACACACACACATCTCCTAATCTTCAAC 642  
 QY 215 LeuGlyLeuGlyTyrGluSerHisAspLeuSerLeu 226  
 DB 643 CTGGAGATGAGATTGTGAGGCCCATGAACCTTCGCTT 678  
 RESULT 8  
 AA257943  
 ID AA257943 standard; cDNA; 924 BP.  
 XX  
 AC AA257943;  
 XX  
 DT 11-APR-2000 (first entry)  
 XX  
 DE Poplar floral homeotic gene PTD cDNA.  
 XX  
 KW Poplar; PTD, floral homeotic gene; transgenic plant; sterility;  
 KW fertility; ss.  
 XX  
 OS Populus balsamifera subsp. trichocarpa.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..684  
 FT CDS /tag= a  
 FT /note= "the coding region is also specifically claimed in  
 Claim 1"  
 XX  
 PN CA2227940-A1.  
 XX  
 PD 06-OCT-1999.  
 XX  
 PF 07-APR-1998; 98CA-02227940.  
 XX  
 PR 06-APR-1998; 98US-00080851.  
 XX  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 PI Rottmann WH, Brunner AM, Sheppard LA, Straus SH;  
 XX WPI; 2000-106662/10.  
 DR P-PSDB; AAY58654.  
 XX  
 PT Nucleic acid from Populus trichocarpa genes, useful for producing  
 PT transgenic plants, particularly trees, with modified fertility  
 PT characteristics such as sterility.  
 XX  
 PS Claim 1; Page 46-47; 92pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding Populus balsamifera subsp.  
 CC trichocarpa PTD protein (see AAY58654). The PTD gene (see AA257942) is 1  
 CC of 4 newly identified floral homeotic genes from this poplar species. It  
 CC is a homologue of DEFICIENS and is expressed strongly in stamen primordia  
 CC from the onset of organogenesis, and is also expressed at low levels in  
 CC carpel primordia. The invention provides nucleic acid sequences of these  
 CC 4 Populus genes, the corresponding cDNA sequences (see AA257942-45) and  
 CC deduced amino acid sequences (see AAY58454-57). It also provides methods  
 CC of using the gene and cDNA sequences to produce genetically engineered  
 CC Populus species and other trees having modified fertility

CC characteristic, including sterility. Genetic constructs useful in  
 CC producing genetically engineered Populus and other trees include  
 CC antisense versions of PTD, dominant negative mutants, and constructs  
 CC useful for gene suppression. Promoter sequences may be used to obtain  
 CC floral specific expression of genes such as cytochrome P450s that may be used  
 CC in genetic ablation strategies to produce trees having modified fertility  
 CC characteristics, including sterility. Sterile trees allow increased wood  
 CC yield and a reduction in the production of allergens such as pollen  
 XX  
 XX Sequence 924 BP; 309 A; 185 C; 201 G; 229 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	4,37e-54	Length:	924
Score:	595.00	Matches:	125
Percent Similarity:	69.83%	Conservative:	37
Best Local Similarity:	53.88%	Mismatches:	58
Query Match:	50.55%	Indels:	12
DB:	3	Gaps:	4

US-10-690-246a-2 (1-227) x ADK59650 (1-924)

QY 1 MetGlyAryGlyIleGluIleGlyLeuIleGluAsnProThrAsnArgGlnValThr 20  
 DB 1 ATGGGTCGTGGAAGATTGAAATCAAGAAATCGAAACCCCAACAGGCAAGTCACC 60  
 QY 21 TyrSerIleAryAryValGlyIleLeuIleValAlaLeuGluLeuThrValLeuCysAsp 40  
 DB 61 TACTCGAAGAAAGAAATGGATTTTCAAGAAAGCCCAAGAACTGACTGATCTTGAT 120  
 QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyIleLeuIleAspTyrCysSerPro 60  
 DB 121 GCTAAGCTCTCTTATCATTTGTCCTCCACACTTAACAACTCAATGATGATTAAGCCC 180  
 QY 61 SerThrAspIleLeuGlyIleTyrGluAryTyrGlnValThrGlyMetAspLeuTyr 80  
 DB 181 TCCACATCGCAAGAAAGATCTGATCATATCATAGAACCTTAAAGCATAGATCTGTGG 240  
 QY 81 AsnAlaGlnTyrGluAryMetGlnAsnThrLeuIleIleLeuAsnGlnAsn 100  
 DB 241 GGCATCATATTCGAAATGCAAGAGACCTTGAGAACTGAAATGATCATCATTAAG 300  
 QY 101 LeuAryGlyLeuIleAryAryValGlyIleGluIleLeuGluIleMetAspIleLeuGln 120  
 DB 301 CTGAGACAGAAATCAAGCAAGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 360  
 QY 121 LeuAryGlyLeuGluIleThrLeuGluIleSerLeuAryIleValAlaGlyIleTyr 140  
 DB 361 CTGGCGGCTCTTGAAGCAATATGATGAAAGCTTGAATGCTGTGCGTGGCAGGAAGTAC 420  
 QY 141 HisValIleAlaThrGlnThrAspThrTyrIleIleValLeuIleIleSerThrAryGluThr 160  
 DB 421 CATGTGATCAAAACAAAGAAACCTACAGAAAGGGAAGAAATTTAAGAGAGAGA 480  
 QY 161 TyrAryAlaLeuIleHisGluLeuAspMetLeuGluIleAsnProAsnTyrGlyPheAsn 180  
 DB 481 CATGGAACCTCTTGATGGAATATGAAAGCAAACTAAGAGATCAAGTATGTTTA--- 537  
 QY 181 ValGluAsnGlnSerAryIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200  
 DB 538 GTGACACAT-----GAAAGCTGCTGTGCACTTGCAAAATGGGGCTTCAC 582  
 QY 201 MetPheSerPheAryValAlaHisProAsnGln-----ProAsnLeu--- 214  
 DB 583 CTCTATGATATTCGCGCTGATCATCGGCGCAACCAACCAACCATTCCTCATCTTCAC 642  
 QY 215 LeuGlyLeuGlyIleTyrGluSerHisAspLeuSerLeu 226  
 DB 643 CTTGAGATGGAATTTGAGAGCCCATGAATCTTGCGCTT 678

RESULT 9  
 ADKS9650  
 ID ADKS9650 standard; DNA; 637 BP.

XX

AC ADK59650;

XX 06-MAY-2004 (first entry)

XX plant DNA sequence which confers altered metabolic characteristic #7033.

XX altered metabolic characteristic; plant; acid metabolism;

XX alcohol metabolism; fatty acid metabolism;

XX branched fatty acid metabolism; alkaloid metabolism;

XX amino acid metabolism; ester metabolism; glyceride metabolism;

XX terpene metabolism; isoprenoid metabolism; alkene metabolism;

XX alkyne metabolism; hydrocarbon metabolism; ketone metabolism;

XX quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

XX Unidentified.

XX WO2003020936-A1.

XX 13-MAR-2003.

XX 30-AUG-2002; 2002WO-US027884.

XX 31-AUG-2001; 2001US-0316471P.

XX (DOWC ) DOW CHEM CO.

XX (DOWC ) DOW AGROSCIENCES LLC.

XX Weglarz T, Gachotte D, Blakelee B, McCreary DA, Pell RJ.

XX Orfiedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;

XX WPI; 2003-313091/30.

XX Novel genes that confer altered metabolic characteristics in Nicotiana

XX benthamiana plants, useful for altering the levels of metabolites e.g.

XX acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

XX claim 1; SEQ ID NO 7033; 2576bp; English.

XX The invention comprises DNA sequences which confer an altered metabolic

XX characteristic when they are expressed in a plant. The DNA sequences of

XX the invention are useful for producing plants with an altered metabolic

XX characteristic, such as: altered acid metabolism, alcohol metabolism,

XX fatty acid metabolism, branched fatty acid metabolism, alkaloid or other

XX base metabolism, altered amino acid metabolism, altered ester metabolism,

XX altered glyceride metabolism, altered phenolic metabolism, altered

XX carbohydrate metabolism, altered sterol, oxygenated terpene, or

XX isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon

XX metabolism, ketone or quinone metabolism. The DNA sequences of the

XX invention may be used to provide disease resistance in a plant and gene

XX shuffling or sexual PCR procedures. The present nucleic acid represents a

XX DNA sequence of the invention.

XX Sequence 637 BP; 155 A; 193 C; 164 G; 125 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	2,94e-52	Length:	637
Score:	576.00 <td>Matches:</td> <td>107 </td>	Matches:	107
Percent Similarity:	84.87% <td>Conservative:</td> <td>22 </td>	Conservative:	22
Best Local Similarity:	70.39% <td>Mismatches:</td> <td>23 </td>	Mismatches:	23
Query Match:	48.94% <td>Indels:</td> <td>0 </td>	Indels:	0
DB:	10 <td>Gaps:</td> <td>0 </td>	Gaps:	0

US-10-690-246a-2 (1-227) x ADK59650 (1-637)

QY 1 MetGlyAryGlyIleGluIleGlyLeuIleGluAsnProThrAsnArgGlnValThr 20

DB 180 ATGGGAGAGGGCAAGATTCAGATCAAGCGGATCGAAGACCCCAACAGGCGAGTGACC 239

QY 21 TyrSerIleAryAryValGlyIleLeuIleValAlaLeuGluLeuThrValLeuCysAsp 40

DB 240 TACTCGAAGCGCGCAAGGAGATCATGAAGAAAGCCCAAGGAGCTCACCGTGTCTGCGAC 299

QY 41 AlAGlnValSerIleuMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60  
 DB 300 GCCCAGGTCCGATCATGATCTCTCTCCACCGGCAAGTACACAGGATCTCGAGCCCT 359  
 QY 61 SerThrAspIleuLeuGlyIleTyrGluArgTyrGlnValAlaThrGlyMetAspLeuTyr 80  
 DB 360 TCCACGACATCAAGGGGATCTTTGACCGCTACACGACCAACCTCGCACCACCTTTGG 419  
 QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysIleLeuAsnGluIleAsnGlnAsn 100  
 DB 420 ATCGACGAGTATGAGATATATGACGCGCATCGTACGATCTCAAGGACATCAACCGCAC 479  
 QY 101 LeuArgLysGluIleLeuArgArgLysGlyGluLeuLysGluMetAspIleLysGln 120  
 DB 480 CTGCGCACCCAGATCAGGCAAGATGCGAAGATCTGACGCGGTGAGTTGACGAG 539  
 QY 121 LeuArgGlyLeuGluGlnThrLeuGluSerLeuArgIleValArgHisArgLysTyr 140  
 DB 540 CTGCGCGGTCTTGAGCAAAATGTCGATCCGCGCTCAAGAGGTTCCGCCACAGAGTAT 599  
 QY 141 HisValIleAlaThrGlnThrAspThrTyrLysLys 152  
 DB 600 CATGTATCAGACACAGACTGAAACCTACAGAAA 635  
 RESULT 10  
 AAD42259 standard; cDNA; 926 BP.  
 AAD42259:  
 AC AAD42259:  
 AT 04-NOV-2002 (first entry)  
 DE Soybean AP3 homologue cDNA from clone sElin.pk001.116.  
 XX  
 KW Floral developmental protein; flowering locus T; APETALA3; transgenic;  
 KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;  
 KW sterility; plant growth; inflorescence architecture; plant morphology;  
 KW tissue culture; cell division; soybean; gene; ss.  
 XX  
 OS Glycine max.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 11..694  
 FT /\*tag= a  
 FT /product= "Soybean AP3 homologue protein"  
 XX  
 PN W0200244390-A2.  
 XX  
 PD 06-JUN-2002.  
 PD  
 PF 21-NOV-2001; 2001WO-US043750.  
 PF  
 PR 28-NOV-2000; 2000US-0253415P.  
 PR  
 XX (DUPO ) DU PONT DE NEMOURS & CO B I.  
 PA Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;  
 PI  
 XX WPI: 2002-547703/58.  
 DR P-PSDB; AAE25757.  
 DR  
 XX New floral developmental polypeptide having flowering locus T or AP3  
 PT homolog activity, useful for immunological screening of cDNA expression  
 PT libraries.  
 XX  
 PS Claim 6; Page 80; 88pp; English.  
 XX  
 CC The present invention relates to novel floral developmental proteins,  
 CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologue  
 CC proteins and polynucleotides encoding such proteins. Floral developmental  
 CC polynucleotides are useful for transforming cells or for producing plants  
 CC by transforming the plant cells with the polynucleotides and regenerating  
 CC the plants from the transformed plant cells. Sequences of the invention

CC are useful for immunological screening of cDNA expression libraries. They  
 CC are also useful for creating transgenic plants. Polynucleotides of the  
 CC invention are used as probes for genetically and physically mapping the  
 CC genes that they are a part of and as markers for traits linked to those  
 CC genes. AP3 homologues may be useful for engineering plant sterility or  
 CC fertility, flower development and morphology. FT or TFL1 homologues are  
 CC useful for engineering flowering time, plant growth rate, inflorescence  
 CC architecture, tissue culture morphology and rate of cell division to  
 CC enhance transformation. The present sequence is soybean AP3 homologue  
 CC cDNA  
 XX  
 SQ Sequence 926 BP; 304 A; 195 C; 194 G; 233 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 4,59e-50 Length: 926  
 Score: 557.50 Matches: 109  
 Percent Similarity: 70.89% Conservative: 42  
 Best Local Similarity: 51.17% Mismatches: 59  
 Query Match: 47.37% Indels: 3  
 DB: 6 Gaps: 3  
 US-10-690-246a-2 (1-227) x AAD42259 (1-926)  
 QY 1 MetGlyArgGlyLysIleGluIleLysIleGluAsnProThrAsnArgGlnValThr 20  
 DB 11 ATGGCTAGAGGAAGATCCAGATCAAGAGATGAGAACACCAACCGCGAGTCACT 70  
 QY 21 TyrSerLysArgArgValGlyIleLeuLysValLysGluLeuThrValLeuCysAsp 40  
 DB 71 TACTCTAACGACGGAATGGCTTTTCAGAAAGCCCAACGAGCTTCCGTTCTCTGGAT 130  
 QY 41 AlAGlnValSerIleuMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60  
 DB 131 GCCAAGGTTCTATATATATGTTCTCCAGCATGGAATACTCAACCATTCATCAAGCCC 190  
 QY 61 SerThrAspIleuLeuGlyIleTyrGluArgTyrGlnValAlaThrGlyMetAspLeuTyr 80  
 DB 191 TCCACCTCAACAAAGCAGTTCTTCGATCATACAGATGACTCGGAGTTGATCTCTGG 250  
 QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysIleLeuAsnGluIleAsnGlnAsn 100  
 DB 251 AACTCATTAACGAAATGATGCAAGAACTTGAAGAACTGAAGAGGTGAATAGCAAT 310  
 QY 101 LeuArgLysGluIleLeuArgArgLysGlyGluLeuLysGluMetAspIleLysGln 120  
 DB 311 CTTCGTAAAGAGATTAGGACAGAAATGGAGATTGTTGAACAGACTGGCATGAAAGAT 370  
 QY 121 LeuArgLysGluGlnThrLeuGluSerLeuArgIleValArgHisArgLysTyr 140  
 DB 371 CTCAAGCTCTTGAGGAAGAAATGACACAGCCCGCAAGTTGTTCTGTAGCGTAACTAT 430  
 QY 141 HisValIleAlaThrGlnThrAspThrTyrLysLysIleLysSerThrArgGluThr 160  
 DB 431 AAGGTATTAACAATCAGATTGACACCCAGAGGAAAGATTATATAACGAAAGAAAGTG 490  
 QY 161 TyrArgAlaLeuLysIleGluLeuAspMetLysGluLysAsnProAsnTyrGlyPheAsn 180  
 DB 491 CACAAACGCTCCGTCGATGATGATGACAAAGCAAGCAATCCACCTTTGCACTG-- 547  
 QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200  
 DB 548 ATGATATATGAGGGGAG--TATGAGTCTGTGATCGGATTCATAATTAGTCCACGC 604  
 QY 201 MetPheSerPheArgValAlaHisProAsnGlnProAsn 213  
 DB 605 ATGTTGCAATTGAGC--ATACAAACCAAGCATCTAGT 640  
 RESULT 11  
 ADR04282 standard; cDNA; 926 BP.  
 ID ADR04282  
 XX ADR04282:  
 AC ADR04282:  
 AT



XX (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 XX  
 PI Deikman J, Peng PCC, Fincher KL, Ziegler TE;  
 XX  
 DR WPI; 2004-479808/45.  
 XX  
 PT New isolated nucleic acid molecule that encodes a plant protein or its  
 PT fragment, useful for isolating a variety of agronomically significant  
 PT genes associated with plant growth, quality or yield, and as molecular  
 PT tags to map genes.  
 XX  
 PS Claim 1; SEQ ID NO 8631; 34pp; English.  
 XX  
 CC The invention relates to 17880 cotton expressed sequence tags (ESTs;  
 CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated  
 CC from primed or non-primed seeds from variety DP50B, mature seeds from  
 CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium  
 CC tissue, developing fibres, carpel walls and septa from variety  
 CC Nuocotton33B. The invention also relates to substantially purified  
 CC proteins or their fragments encoded by nucleic acid molecules of the  
 CC invention, and to transformed plants having a nucleic acid construct  
 CC comprising a nucleic acid of the invention. The cotton ESTs are useful as  
 CC molecular tags to isolate genetic regions, to isolate genes, to map  
 CC genes, to determine gene function and to determine whether genes are  
 CC members of a particular gene family. The nucleic acid molecules may be  
 CC used for isolating a variety of agronomically significant genes  
 CC associated with plant growth, quality, yield, and could also serve as  
 CC links in metabolic and catabolic pathways. The nucleic acid molecules are  
 CC also useful for identifying genes important in initiating and maintaining  
 CC seed germination or that may be used to mitigate stresses encountered  
 CC during seed germination. The ESTs additionally enable the acquisition of  
 CC promoters and cis-regulatory elements which will be useful to express  
 CC agronomically significant genes in these tissues and/or other tissues,  
 CC and also permits the acquisition of molecular markers useful in breeding  
 CC schemes, genetic and molecular mapping, and in cloning of agronomically  
 CC significant genes. The nucleic acid molecules are further useful for  
 CC detecting the expression level or pattern of a protein or mRNA and for  
 CC detecting the presence or quantity of a protein by tissue printing. The  
 CC present sequence represents a specifically claimed EST isolated from a  
 CC cotton variety Nuocotton33B androecium tissue cDNA library (1B3828). The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from the US  
 CC patent office at seqdata.uspto.gov/sequence.html?docID=US20040123340  
 CC  
 XX  
 SQ Sequence 644 BP; 214 A; 120 C; 150 G; 158 T; 0 U; 2 Other;

Alignment Scores:  
 Pred. No.: 3,699-47 Length: 644  
 Score: 528.50 Matches: 108  
 Percent Similarity: 71.84% Conservative: 40  
 Best Local Similarity: 52.43% Mismatches: 56  
 Query Match: 44.90% Indels: 3  
 DB: 13 Gaps: 2

US-10-690-246a-2 (1-227) x ACN53850 (1-644)

QY 1 MetGlyArgGlyIleGluIleGlySerIleGluAsnProThrAsnArgGlnValThr 20  
 DB 32 ATGGCTCAGGAGGAGATCAATCAATCAAGCTGATAGAGAACTGACCAACAGGCAATCAAG 91  
 QY 21 TyrSerIleValArgValGlyIleLeuIleValAlaIleValGluLeuThrValLeuGlyAsp 40  
 DB 92 TATTCGAAAGAGAAAGACGGCTCTTTCAGAAAGCTAATGAACTTACAGTTCTTGGCAT 151  
 QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyIleValLeuAlaAspTyrCysSerPro 60  
 DB 152 GCTAAGGTTTCATCATCATGTTTTCACCTACTGTTAACTCAACAGAGTTTACAGCCCT 211  
 QY 61 SerThrAspIleValGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr 80

DB 212 TCACCAACACAGAGAGAGATTAATTCATGATACGATACAGAAACCTTGGGATTCGATATCTGG 271  
 QY 81 AsnAlaGlnIleTyrGluArgMetGlnAsnThrIleuIleValGlnGluIleAsnGlnAsn 100  
 DB 272 AACACCCACTATGAGAAATGCAAGACAGCTTGAAGACACTGAAAGAGGTTTAAACAGAAC 331  
 QY 101 LeuArgIleGluIleLeuArgArgIleGlyGluIleGluGluIleMetAspIleValGln 120  
 DB 332 CTGCGGAAAGAGATTGAGAGAGATGGCGACTGTTTGAATGATTGACATCAAGAT 391  
 QY 121 LeuArgGlyLeuGluIleThrLeuGluGluIleSerLeuArgIleValArgIleValGly 140  
 DB 392 CTGGTGCTTGGAAACAAAGAAATGAGAGACTCTGTCACTTATTCGTATTAAGATAT 451  
 QY 141 HisValIleLeuIleThrIleThrAspThrTyrIleValLeuLeuIleValSerThrArgIle 160  
 DB 452 CGTGTCTCTCCAAACAGATCGATCTTCACAGAAAGAGTGAATGTGAAAGATTA 511  
 QY 161 TyrArgIleLeuIleIleGluLeuAspMetIleValGluIleValProAsnTyrGlyPheAsn 180  
 DB 512 CACAAAATCTCTTACATGAACTGGAATCCCTGAAAGAAAGATCA--TATGGAATTA-- 566  
 QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200  
 DB 567 GTTGATTAATGAGAGCGGAT--TATGATACCCCTGATCGGATTAATAATGAGAGTCTCTGT 623  
 QY 201 MetPheSerPheArgVal 206  
 DB 624 ATATTTCCTTACGCCCTG 641

RESULT 13  
 AA051189  
 ID AA051189 standard; DNA; 882 BP.  
 XX  
 AC AA051189;  
 DT 25-MAR-2003 (revised)  
 DT 19-JUN-1994 (first entry)  
 XX  
 DE Homeotic gene green petal.  
 XX  
 KW Plant; organ morphogenesis; control; petunia; petals; ss.  
 XX  
 OS Petunia.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 17..713  
 FT CDS /\*tag= a  
 XX  
 PN MO9321322-A1.  
 PN XX  
 PD 28-OCT-1993.  
 PD XX  
 PE 13-APR-1993; 93WO-US003508.  
 PE XX  
 PR 13-APR-1992; 92US-00867580.  
 PR XX  
 PR 06-JUL-1992; 92US-00909589.  
 PR XX  
 PA (UTRQ ) UNIV ROCKEFELLER.  
 PI Halfter U, Van Der Krol AR, Kush A, Chua N;  
 DR WPI; 1993-351732/44.  
 DR P-PSDB; AAR43385.  
 XX  
 PT Plant organ morphogenesis control and determ. - by regulating the  
 PT expression of homeotic genes which determine the identity of the organ.  
 XX  
 PS Claim 13; Fig 2; 74pp; English.  
 CC The homeotic gene green petal from petunia has been cloned and  
 CC characterised previously. The gene was used in a new method for





Db 514 CATAGAAATCTCTTGGCTTGATTTGATGCAAGACAGAGGACCA-----TATCGA 564  
QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200  
Db 565 TTGGTTGAGCAGAGAGGGGACTATAACTCTGTGCTTGATTTCCCAATGGAGGGCCACGC 624  
QY 201 Met 201  
Db 625 ATA 627

Search completed: October 6, 2005, 13:09:50  
Job time : 568 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 6, 2005, 12:43:06 ; Search time 3342 Seconds  
(without alignments)  
2585.455 Million cell updates/sec

Title: US-10-690-246A-2

Perfect score: 1177

Sequence: 1 MGRGKIKIKIENPTNRQVT.....HPNQPLIGIKYSHDLSLA 227

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgr2\_1/USFPO\_spool/US10690246/runat\_05102005\_110910\_6447/app\_query.fasta\_1.391  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	57.3	872	6	CD439730 EL01N0528
2	675	57.3	1273	3	AY109302 Zea mays
3	621	52.8	694	6	CB921382 VVD07008
4	618	52.5	585	6	CB626851 OS11B01G
5	588	50.0	645	2	BE497689 WHE955.D0
6	587.5	49.9	710	5	BU875031 V001F01.P
7	578	48.1	651	5	BU994760 HM08C02+
8	576	48.9	615	7	CO997489 11u01-6ms
9	573	48.7	762	6	CB971393 CAB10005_

10	570.5	48.5	639	5	BU879075	BU879075 V055E10.P
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15	555.5	47.2	591	7	CO995351	CO995351 eca01-5cs
16	553.5	47.0	650	7	CV005022	CV005022 eca01-13c
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20	547	46.5	605	6	CA597172	CA597172 wpa1c.pk0
21	538	45.7	532	2	BF291839	BF291839 WHE2204.E
22	536	45.5	630	6	CA600487	CA600487 waw1c.pk0
23	534	45.4	508	5	BU878141	BU878141 V043F04.P
24	534	45.4	757	1	AJ568207	AJ568207 AJ568207
25	533	45.3	697	1	AJ568191	AJ568191 AJ568191
26	533	45.3	722	1	AJ559554	AJ559554 AJ559554
27	533	45.3	762	1	AJ799190	AJ799190 AJ799190
28	533	45.3	784	1	AJ790416	AJ790416 AJ790416
29	524	44.5	689	7	CO106481	CO106481 GR_EB003
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31	522	44.4	724	7	CO123447	CO123447 GR_EB05J
32	521.5	44.3	868	7	CV505838	CV505838 72490.1.M
33	521	44.3	581	5	BU880121	BU880121 UM411P12
34	515.5	43.8	717	6	CD838295	CD838295 RF02.110K
35	514.5	43.7	660	7	CV516063	CV516063 0048P0012
36	514.5	43.7	691	7	CV516051	CV516051 0048P0012
37	514.5	43.7	666	7	CV516589	CV516589 0048P0015
38	514	43.7	682	7	CV515313	CV515313 0048P0008
39	511	43.4	616	2	BF324502	BF324502 eu12902.Y
40	511	43.4	623	1	AJ801669	AJ801669 AJ801669
41	508.5	43.2	871	3	CNS0A722	BX823171 Arabidops
42	507	43.1	714	4	BI929568	BI929568 EST549457
43	506.5	43.0	624	7	CK118415	CK118415 217b1.P1
44	506.5	43.0	704	7	CV295468	CV295468 EST883845
45	506.5	43.0	969	3	CNS09YEQ	BX842104 Arabidops

#### ALIGNMENTS

RESULT 1  
LOCUS CD439730 872 bp mRNA linear EST 03-JUN-2003  
DEFINITION EL01N0528D01.b EndospERM\_5 Zea mays cDNA, mRNA sequence.  
ACCESSION CD439730  
VERSION CD439730.1 GI:31355373  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 872)

AUTHORS Lai J., Dey N., Kim C.S., Bharti A.K., Rudd S., Mayer K.F.,

Larkins B., Becraft P. and Messing J.

TITLE Characterization of the maize endospERM transcriptome and its comparison to the rice genome

JOURNAL Genome Res. 14 (10), 1932-1937 (2004)

COMMENT Contact: Lai, Jinseng

Dr. Joachim Messing's lab

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190 Frelinghuysen Rd., Piscataway, NJ 08854, USA

Tel: 732-445-3801

Fax: 732-445-5735

Email: jlai@wakeman.rutgers.edu

Seq primer: T3.

FEATURES  
source location/Qualifiers  
1..872  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultiivar="W22"  
/db\_xref="taxon:4577"  
/feature\_type="EndospERM of 7-23DAP"







Qy 61 SerThrAspIleYsglyIleTyrgluArgIValValThrGlyMetAspLeuTrp 80  
 |||||  
 |||||  
 Db 288 GGCACGACATCAAGGGGATCTTTGACCGCTACAGAGGCACTGGACCAAGCTGTGG 347  
 |||||  
 Qy 81 AsnAlaGlnTyrgluArgMetGlnAsnThrLeuLeuHisIleuAsnGlnIleAsnGln 100  
 |||||  
 |||||  
 Db 348 ATCAGACAGATATAGATATAGACCGCACCTGACATCTCAAGACATCAATCCGAC 407  
 |||||  
 Qy 101 LeuArgLyseGluIleArgArgIValGluGluIleuGluGlyMetAspIleYsgln 120  
 |||||  
 |||||  
 Db 408 CTCGCGACCGAGATC-----AGATGGGTGAGATCTGACCGCGCTGAGATTGAGAG 461  
 |||||  
 Qy 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgIleYr 140  
 |||||  
 |||||  
 Db 462 CTCGCGACACTTGAGCAAAATGTCATCGCTCTCAAGAGGTTCCGACAGAGATAT 521  
 |||||  
 Qy 141 HisValIleAlaThrGlnThrAspThrTyrglyLeuLeuYsglyMetAspIleYsgln 160  
 |||||  
 |||||  
 Db 522 CATGTGATCACACGACGACTGAAACCTACAGAGAGGTGAGACCTCCAGAGAGCA 581  
 |||||  
 Qy 161 TyrArgAlaLeuIleHisGluLeuAspMetLeuGluIleuAsnProAsnTyrglyPheAsn 180  
 |||||  
 |||||  
 Db 582 TACAGAAATCTGCAGCAGAGCTGGTATGCGCAGAGAC---CCGGCGTACGGTTTC--- 635  
 |||||  
 Qy 181 ValGluAsn 183  
 |||||  
 Db 636 GTGGACAC 644

RESULT 6  
 BU875031 710 bp mRNA linear EST 16-OCT-2002  
 LOCUS BU875031  
 DEFINITION V001F01 Populus flower cDNA library Populus balsamifera subsp.  
 trichocarpa cDNA 5 prime, mRNA sequence.

ACCESSION BU875031 GI:24066555  
 VERSION BU875031.1  
 KEYWORDS EST.  
 SOURCE Populus balsamifera subsp. trichocarpa (Populus trichocarpa)  
 ORGANISM Populus balsamifera subsp. trichocarpa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosid 1; Malpighiales; Salicaceae; Salicaceae; Populus.

REFERENCE 1 (bases 1 to 710)  
 Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
 The poplar tree transcriptome: Analysis of expressed sequence tags  
 from multiple libraries

JOURNAL Unpublished (2002)  
 COMMENT Contact: BHADERAO RUPALI R.  
 Umea Plant Science Center  
 Department of Plant Physiology  
 University of Umea, 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalerao@plantphys.umu.se.

FEATURES  
 source Location/Qualifiers

1..710  
 /organism="Populus balsamifera subsp. trichocarpa"  
 /mol\_type="mRNA"  
 /sub\_species="trichocarpa"  
 /db\_xref="taxon:3694"  
 /tissue\_type="floral buds"  
 /clone\_lib="Populus flower cDNA library"  
 /note="Organ: flower"

ORIGIN

Alignment Scores:  
 Pred. No.: 3.1e-59 Length: 710  
 Score: 587.50 Matches: 121  
 Percent Similarity: 69.37% Conservative: 33  
 Best Local Similarity: 54.50% Mismatches: 53  
 Query Match: 49.92% Indels: 15  
 DB: 5 Gaps: 3

US-10-690-246A-2 (1-227) x BU875031 (1-710)

Qy 1 MetGlyArgGlyLyseIleGluIleYsglyIleGluAsnProThrAsnArgIValThr 20  
 |||||  
 |||||  
 Db 85 ATGGGTCTGTGAAAGATGAAATGCAAGAGATCGAAGAACCCAGAAAGGCAAGCACC 144  
 |||||  
 Qy 21 TyrSerIleArgArgValGlyIleLeuYsglyAlaYsglyIleuThrValIleuCyAsp 40  
 |||||  
 |||||  
 Db 145 TACTCGAAGAGAAATGATGATTTTTCAGAAAGCCCAAGAACTGACTGACTTGTGAT 204  
 |||||  
 Qy 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLyseValAlaAspTyrcysSerPro 60  
 |||||  
 |||||  
 Db 205 GCTAAGTCTCTTATCATGTTCTTCAACATCAACAACTCAATGATGATATACCCCC 264  
 |||||  
 Qy 61 SerThrAspIleYsglyIleTyrgluArgIValValThrGlyMetAspLeuTrp 80  
 |||||  
 |||||  
 Db 265 TCCACATTCACAAAGAAATGATCAAGTCAATTCAGAACGCTTGAAGCATATGCTGTGG 324  
 |||||  
 Qy 81 AsnAlaGlnTyrgluArgMetGlnAsnThrLeuLeuHisIleuAsnGlnIleAsnGln 100  
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 |||||  
 Db 325 GGCACCTCAATACAGAAATGCAAGACCTTGAGAGACTGAAATGATCAATCATTAAG 384  
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 Qy 101 LeuArgLyseGluIleArgArgIValGluGluIleuGluGlyMetAspIleYsgln 120  
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 |||||  
 Db 385 CTGAGACAGAAATTCAGCAGAGAGAGAGAGGCGCTGAATGATCTGAGCATTGATCAT 444  
 |||||  
 Qy 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgIleYr 140  
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 |||||  
 Db 445 CTCGCGGCTTTCAGCAACATATGACTGAAGCCTTGAATGTGTGCGCAGAGAGTAC 504  
 |||||  
 Qy 141 HisValIleAlaThrGlnThrAspThrTyrglyLeuLeuYsglyMetAspIleYsgln 160  
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 |||||  
 Db 505 CATGTATCAAAACACAAACGAAACCTACAGAGAGGTGAGAAATTTAGAGAGACA 564  
 |||||  
 Qy 161 TyrArgAlaLeuIleHisGluLeuAspMetLeuGluIleuAsnProAsnTyrglyPheAsn 180  
 |||||  
 |||||  
 Db 565 CATGGAACCTCTTGATGATGAAATGAAAGCAAACTGAGAGATGACATGATGTTTA--- 621  
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 Qy 181 ValGluAsnGlnSerArgIleTyrgluAsnSerIleProMetValIleGluCySPProGln 200  
 |||||  
 |||||  
 Db 622 GTGGACAT-----GAAGCGCTGTTGCACTTCGAATGGGCGCTTCCAC 666  
 |||||  
 Qy 201 MetPheSerThrArgValValHisProAsnGlnProAsnLeuGluGlyLeuGlu 220  
 |||||  
 |||||  
 Db 667 CTTATGCAATTCGCTGCATCAC-----GGGACAC 699  
 |||||  
 Qy 221 SerHis 222  
 |||||  
 Db 700 CACCAC 705

RESULT 7  
 BU994760 651 bp mRNA linear EST 23-OCT-2002  
 LOCUS BU994760  
 DEFINITION HM08C02r HM Hordeum vulgare subsp. vulgare cDNA clone HM08C02  
 5-PRIME, mRNA sequence.

ACCESSION BU994760 GI:24271743  
 VERSION BU994760  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Trilicaceae; Hordeum.

REFERENCE 1 (bases 1 to 651)  
 Zhang, H., Meschke, W., Michalek, W., Stein, N. and Graner, A.  
 EST sequencing and analysis in barley (2002)

JOURNAL Unpublished (2002)  
 COMMENT Contact: Stein Nils  
 Molecular Markers Group, Department Genbank  
 Institute of Plant Genetics and Crop Plant Research (IPK)  
 Corrensstr. 3, 06466, Gatersleben, Germany  
 Tel: 039482-5522  
 Fax: 039482-5595



Db 202 GCTGAGTTTCTCTCATGTTTCCAGACACTGGGAAATTCCTGATATTGACGCCCT 261  
 Qy 61 SerThrAspIleLeuGlyIleTyrGluArgTyrGlnValAlaThrGlyMetAspLeuTTP 80  
 Db 262 TCTACACAGCAGAAAGATTTTCATCGTTTACAGCAAGATTTCAGGACAGACTTATG 321  
 Qy 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLeuHisIleuAsnGluIleAsnGlnAsn 100  
 Db 322 AACCTTCACATCAACAGAAATTTAGAAAGTTTATCAAAAGTTGTCGCAAGAGATAT 361  
 Qy 101 LeuArgGlyGluIleArgArgGlyGlyGluGluLeuGluGlyMetAspIleLeuGln 120  
 Db 382 CTCGGAGGCGCAATCAGGCAATGAGATCGTGAAGATTCGACCATCTCGAAATCGAAGA 441  
 Qy 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgGlyTyr 140  
 Db 442 CTCGCGCGCTTTAGCAAAATTTAGAAAGTTTATCAAAAGTTGTCGCAAGAGATAT 501  
 Qy 141 HisValIleAlaThrGlnThrAspThrTyrIleLeuLeuLeuLeuSerThrArgGluThr 160  
 Db 502 CATGTGATCAACACTCAAAAGAGACTTACAGAAAGTTGAGAACTTGCAAGAGCA 561  
 Qy 161 TyrArgAlaLeuLeuHisGluLeu 168  
 Db 562 CACGCAAAATTTTATTCGGAATTG 585

RESULT 9  
 CB971393 762 bp mRNA linear EST 30-APR-2003  
 LOCUS CB971393

DEFINITION CAB10005.1ta\_Fa\_B07 Cabernet Sauvignon Flower Pre-bloom - CAB1  
 vitis vinifera cDNA clone CAB10005.1ta\_Fa\_B07 5', mRNA sequence.

ACCESSION CB971393.1 GI:30254946  
 VERSION CB971393  
 KEYWORDS EST.

SOURCE Vitis vinifera  
 ORGANISM Vitis vinifera

REFERENCE Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J.,  
 Jones, K. and Cook, D.  
 Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'  
 berries at various developmental stages  
 Unpublished (2003)

JOURNAL CONTACT: Douglas Cook, PhD  
 CAES Genome Facility  
 UC Davis, Plant Pathology  
 One Shields Ave, Davis, CA 95616, USA  
 Tel: 530 754 6561  
 Fax: 530 754 6617  
 Email: drcocok@ucdavis.edu  
 Seq primer: ACGGTACCGGACATATGCC.

FEATURES  
 source  
 1..762  
 Location/Qualifiers

/organism="Vitis vinifera"  
 /mol\_type="mRNA"  
 /cultivar="Cabernet Sauvignon"  
 /db\_xref="taxon:29760"  
 /clone="CAB10005.1ta\_Fa\_B07"  
 /sex="Hermaphrodite"  
 /dev\_stage="Pre-bloom"  
 /lab\_host="DHSalpha"  
 /clone\_lib="Cabernet Sauvignon Flower Pre-bloom - CAB1"  
 /note="Organ: Flower - Pre-bloom; Vector: pNR; Site\_1:  
 Site\_2: Site\_1; CAB1 is a cDNA library of Vitis  
 vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples  
 were collected approximately eleven days before onset of  
 bloom (clusters at this stage were fully developed and  
 flowers with calypters or caps still attached. Sampled  
 vines were located at the University of California, Davis,  
 experimental vineyard. cDNAs were made by oligo-dT priming  
 and directionally cloned. 5' and 3' adaptors were used in

cloning as follows:  
 5'-AAGCAGTGTATCAACGAGAGGCGCATTTACGGCGG-3' and  
 5'-ATTCTAGAGCCGAGGCGGCGGACATG-dt(30)NN-3'. Library was  
 constructed using the Clontech Creator SMART kit and  
 size-selected to contain the 0.5-3 kb size fraction."

# ORIGIN

## Alignment Scores:

Pred. No.:	1,82e-57	Length:	762
Score:	573.00	Matches:	119
Percent Similarity:	70.22%	Conservative:	39
Best Local Similarity:	52.89%	Mismatches:	63
Query Match:	48.68%	Indels:	4
DB:	6	Gaps:	4

US-10-690-246a-2 (1-227) x CB971393 (1-762)

Qy 1 MetGlyArgGlyLeuGluIleGlyIleGlyIleGluAsnProThrAsnArgGlnValThr 20  
 Db 10 ATGGCTAGAGGAAAGATTGAGATCAAGAGATGAGAACTCGAACAGGCGATCACC 69  
 Qy 21 TyrSerIysArgArgValGlyIleLeuLeuValAlaGlyGluLeuThrValLeuCy6Asp 40  
 Db 70 TACTCCAAAGAGCAAAATGATCTTCAAGAGCGCAGTGAAGCTCACTGTTCTTGTGAT 129  
 Qy 41 AlaglnValSerIleuLeuMetPheSerSerThrGlyIleLeuAlaAspTyrCySerPro 60  
 Db 130 GCTAAGGTTCTATCATCATGCTCTCCAGACTGAGAAAGCTCCATGATATCATCAAGCTT 189  
 Qy 61 SerThrAspIleLeuGlyIleTyrGluArgTyrGlnValAlaThrGlyMetAspLeuTTP 80  
 Db 190 TCCACTACACAGAAACAAATTTGATCATGATACAGAAACCTCTAGAGATGATCTATG 249  
 Qy 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLeuHisIleuAsnGluIleAsnGlnAsn 100  
 Db 250 AGCTATCATATGAGAAATGAGCAAGAAACCTGAGAAAGTGTGAACAGAAAT 309  
 Qy 101 LeuArgGlyGluIleArgArgGlyGlyGluGluLeuGluGlyMetAspIleLeuGln 120  
 Db 310 CTCAGGAAGAGATTAGGCAAGAGATGGTGAACATTGACGATTTGAGCGTTGAGGAA 369  
 Qy 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgGlyTyr 140  
 Db 370 CTGGGAGATCTTGAACAAGATGAGAGATCTTTGAAGATGTTCTGTATAGGAAGTAC 429  
 Qy 141 HisValIleAlaThrGlnThrAspThrTyrIleLeuLeuLeuSerThrArgGluThr 160  
 Db 430 CAGGTGATCAATATATCATGATGAACCTTCAAGAAAGTTAAGAAATGTGAACAATA 489  
 Qy 161 TyrArgAlaLeuLeuHisGluLeuAspMetLeuGlyGluLeuProAsnTyrGlyPheAsn 180  
 Db 490 CACAAATATCTCCATCAATGATTTGATGACAGAGGACGAGATCAATCATATCTATGCTA 546  
 Qy 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCyProGln 200  
 Db 547 GTGACATATGAGGGGAT---TACGAATCTGTTCTTGAATTTCTAAATGAAAGTCTCCG 603  
 Qy 201 MetPheSerPheArgValAlaHisProAsnGlnProAsnLeuLeuGlyIleGlyTyrGlu 220  
 Db 604 GTATTTCCTCAAC---TTGACACCTTAACCCGCTATATGATCTTCACTGGGTGGGC 660  
 Qy 221 SerHisAspLeuSer 225  
 Db 661 TCT---GATTGACC 672

## RESULT 10

BUB79075 639 bp mRNA linear EST 16-OCT-2002  
 LOCUS BUB79075  
 DEFINITION V055E10 Populus flower cDNA library Populus balsamifera subsp.  
 trichocarpa cDNA 5 prime, mRNA sequence.  
 ACCESSION BUB79075  
 VERSION BUB79075.1 GI:24070599  
 KEYWORDS EST.

SOURCE	Populus balsamifera subsp. trichocarpa (Populus trichocarpa)					
ORGANISM	Populus balsamifera subsp. trichocarpa					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
	rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.					
REFERENCE	1. (bases 1 to 639)					
AUTHORS	Umeberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.					
TITLE	The poplar tree transcriptome: Analysis of expressed sequence tags					
JOURNAL	from multiple libraries					
COMMENT	Unpublished (2002)					
	Contact: BHALERAO RUPALI R.					
	Umea Plant Science Center					
	University of Umea, 901 87 Umea, Sweden					
	Tel.: +46 90 786 5279					
	Fax: +46 90 786 6676					
	Email: rupali.bhalerao@plantphys.umu.se.					
FEATURES	location/Qualifiers					
SOURCE	1..639					
	/organism="Populus balsamifera subsp. trichocarpa"					
	/mol_type="mRNA"					
	/sub_species="trichocarpa"					
	/db_xref="taxon:3694"					
	/cissue_type="floral buds"					
	/clone_lib="Populus flower cDNA library"					
	/note="Organ: flower"					
ORIGIN						
Alignment Scores:						
Pred. No.:	2.84e-57	Length:	639			
Score:	570.50	Matches:	114			
Percent Simlilarity:	75.94%	Conservative:	28			
Best Local Simlilarity:	60.96%	Mismatches:	44			
Query Match:	48.47%	Indels:	1			
DB:	5	Gaps:	1			
US-10-690-246A-2 (1-227) x BU879075 (1-639)						
Dn	1	MecGLVARGSLYLSILIEGILLIETLYSLYLEGLIAENPCTHRAASRGIVALTNR	20			
Dn	71	ATGGGTGCTGGAAAGATTGAATCAAGAAGATCGAAAACCCACAACAGGCAGTACC	130			
Dn	21	TyrSerLysArgArgValGlyLeuLeuLysValAlaLysValLeuThrValLeuCysAsp	40			
Dn	131	TACTCGAAGAGAAATGATGTTTCAGAAAGGCCCAAAGCTCATGCTTGAT	180			
Dn	41	ALAGLVALSERILEULEMETPHESRSERTNGLYSLLEALAASPTCYSSERPRO	60			
Dn	191	GCTAAGGCTCTCTTTCATGATGTTCTCCAACCTTAACAACTCAATGATCATTTAGCCC	256			
Dn	61	SeRThrsPrlleYsgLIyleTYrgLUARGYrGLINvalIThrGLMeAsPLeuTrp	80			
Dn	251	TCCACATCGACAAAGAAGATCTRCATCAATTCAGAACGCTTTAGGATGATCTGTGG	310			
Dn	81	ASNlaGLINTyGLIuaRgMetGLInaENThrLeuLySHILEuENGluILEaNglnaSN	100			
Dn	311	GGCACATAATACAGAAATATGCAAGAGCACTTAGAGGAAGCTGAATGATCATCATAG	370			
Dn	101	LeuArGLySGluILEarGARgarGLySGLYglUGluLeuGLUGlyMeAsPRLyELgLn	120			
Dn	371	CTAGAGCAAAATAATCAAGCAGAGGAAGAGGGGCTGAATGATCTGACATTCATCAT	430			
Dn	121	LeuArGLYLeuGLIGlnIThrLeuGLIGluISerLeuArGLILEVALrGHlaRGLyETR	140			
Dn	431	CTGGCGGCTTTAGCAACATAGACTGAAGGCTTGAATGGTGTGCGGSCAGGAAGTAC	490			
Dn	141	HlaVALIlleaIThrGLInThrsPRTThRYtLYSLySLySErThrsArgGLUTHR	160			
Dn	491	CATGTGATCAAAACACAAACGAACCTTCAGAGGAAGAGGTGAANAATTTAGAGAGAGA	550			
Dn	161	TyArGRglaleuLleHISGLIUeaSPMetCLySGLUglUAenPRofaENTYrGLYPhaSN	180			
Dn	551	CATGGAACCTCTTGATGGAATTTGAAGCAAAACTAGAGGATTCGACAGTATAGTGTTTA---	607			

QY	181	ValGluuengInserArgile	187	
Db	608	GTGGACATATGAAGCTGCTGT	628	
RESULT 11				
LOCUS	AW737915		698 bp	mRNA linear EST 18-MAY-2001
DEFINITION	ES1333342 tomato flower buds, anthesis, Cornell University			
ACCESSION	Lycopersicon esculentum cDNA clone CT04121 5', mRNA sequence.			
VERSION	AW737915			
KEYWORDS	AW737915.1 GI:7646860			
SOURCE	EST.			
ORGANISM	Lycopersicon esculentum (tomato)			
REFERENCE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 698)			
AUTHORS	van der Hoeven, R.S., Bezzerides, J.L., Matern, A.L., Holt, I.B., Huang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Roming, C.M., Nierman, W., Frazer, C.M., Martin, G.B., Giovannoni, J.U. and Tanksley, S.D.			
TITLE	Generation of ESTs from tomato flower tissue, anthesis			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a> 5 prime sequence.			
FEATURES	location/Qualifiers			
SOURCE	1..698 /organism="Lycopersicon esculentum" /mol_type="mRNA" /cultivar="TA496" /db_xref="taxon:4081" /clone="CT04121" /clone="CT04121" /db_xref="taxon:4081" /feature="anthesis" /feature="anthesis" /clone_id="tomato flower buds, anthesis, Cornell University" /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Tanksley; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."			
ORIGIN				
Alignment Scores:				
Pred. No.:	4.84e-57	Length:	698	
Score:	569.00	Matches:	117	
Percent Similarity:	69.30%	Conservative:	41	
Best Local Similarity:	51.32%	Mismatches:	64	
Query Match:	48.34%	Indels:	6	
DB:	2	Gaps:	4	
US-10-690-246A-2 (1-227) x AW737915 (1-698)				
QY	2	GlyAArgGlyLysIleGluIleLysIleGluAsnProThrAsnArgGlnValThrTyr	21	
Db	3	GGCGCTGGAAAAATTTGATCAAGAGATTGAAATCGACAAACAGCAGGTCACTTAC	62	
QY	22	SeTlyAArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValIleuCyaaPALA	41	
Db	63	TCCAAAGGAAGAAACGGTATTTTCACAAAGCTAAACAACTTACTGTTCTTGGAGCGCT	122	
QY	42	GlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerProSer	61	
Db	123	AAAGTCTCTCTCATCTCATCTCATCAAGCAACGAGAGATCATGATGATCAACAGCCCAAC	182	
QY	62	ThraPleLysGlyLysIleTyrGlnValArgTyrGlnValValThrGlyMetAspLeuTyrPaa	81	



Db	183	ACTAGCAAAAAGATGATGATGATCATGATGAGATGACTTGGAGTGGATATCTGAGC	242
Qy	82	AlaGlnTyrGluArgMetGlnAsnThrLeuTyrSleuAsnGluIleAsnGlnAsnLeu	101
Db	243	ATTCACTACGAGAAAATGCAAGAAAATCTTGAAAGAGATTGAAAGAGATCAATACAGCTA	302
Qy	102	ArgTysGluIleArgArgArgTysGlyGluGluLeuGluGluGlyMetAspIleTysGlnLeu	121
Db	303	AGAGAGAGATTAAGCAGAGAAACAGGGAGACATGACCGGACTAAATTTTGCAGAGACTA	362
Qy	122	ArgGlyLeuGluGlnThrLeuGluGluGlnSerLeuArgIleValArgHisArgTyrHis	141
Db	363	TGTCACTTGCAGAGAACATCATCTGAATCTGTCTGAGATTCTGAAAGAAAGTACAC	422
Qy	142	ValIleAlaThrGlnThrAspThrTyrIleTyrSlyLeuSlySerThrArgGluThrTyr	161
Db	423	GTCATCAAGATCAACACAGACACTGCAAGAAAGAGGAGGAACTTAGAAGACCAAT	482
Qy	162	ArgAlaLeuIleHisGluLeuAspMetTysGluGluAsnProAsnTyrGlyPheAsnVal	181
Db	483	GGAAACCTTGTACTTGATGGACCAAAATGTGAAGATCCAAAGTATGGTGT--GTG	539
Qy	182	GluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGlnMet	201
Db	540	GAAATGAGGGGCAT--TACCACCTCTGTCGGCATTTGGAAATGAGAGTACACAATCTT	596
Qy	202	PheSerPheArgVal-----ValHisProAsnGlnProAsnLeuGlyLeuGlyTyr	219
Db	597	TATGCTTTTGGCTTCAACACATGACACCCCAATCTTCAAAACGAAAGAGATTTGGT---	653
Qy	220	GluSerHisAspLeuSerLeuAla	227
Db	654	---TCTCGTGAATCAAGTCTCTCC	674

RESULT 12					
BU877396					
LOCUS	BU877396	605 bp	mRNA	linear	EST 16-OCT-2002
DEFINITION	V033E07 Populus flower cDNA library Populus balsamifera subsp. trichocarpa cDNA 5 prime, mRNA sequence.				

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE
<p>           BU0877396            BU0877396.1            GI:24068920            EST.            Populus balsamifera subsp. trichocarpa (Populus trichocarpa)            Populus balsamifera subsp. trichocarpa            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;            rosids; eucosids I; Malpighiales; Salicaceae; Salicaceae; Populus.         </p>	<p>           1 (bases 1 to 605)            Umeberg, P., Bhalerao, R.R., Jansson, S. and Skerly, F.            The poplar tree transcriptome: Analysis of expressed sequence tags            from multiple libraries         </p>

**JOURNAL COMMENT**  
Unpublished (2002)  
Contact: BHALERAO RUPALI R.  
Department of Science, Government of India

**FEATURES**

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Tel: +46 90 786 5279  
Fax: +46 90 786 6676  
Email: rupali.bhalerao@plantphys.umu.se.  
Location/Qualifiers

```

source
1. 605
/organism="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub_species="trichocarpa"
/db_xref="taxon:3694"
/tissue_type="floral buds"
/clone_lib="Populus flower cDNA library"
/note="Organ: flower"

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ORIGIN	Alignment Scores:	length:
Pred. No.:	3.56e-56	605
Score:	561.00	Matches:
		111

Percent Similarity:	76.40%	Conservative:	2
Best Local Similarity:	62.38%	Mismatches:	0
Query Match:	47.66%	Indels:	0
DB:	5	Gaps:	0

US-10-690-246A-2 (1-227) x BU877396 (1-605)

Qy 1 MetGlyArgGlyLysIleGluIleLysLysIleGluAsnProThrAsnArgGlnValThr 20  
:::  
Db 15 TTGGGTCGTGAAAGATTGAATCAAGAGATGAAACCCCAACAACGCAAGTCACC 74

QY 21 TyrSerLysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCysAsp 40

Db 75 TACTCGAAGAGAAGAAATGGTATTTTCAGAAAGCCCAAGACTCAGTACTTGTGTAT 13

Db 135 GCTAAGTCTCTTATCATGTTCTCCACACTACAACTCAATGATGACATTAGCCCC 15

61 SerThrAspIleLeuGlyIleLeuArgLysGlnValValThrGlyMetAspLeuTrp 80

Db 195 TCACATCGACMAGAATCTACGATCATATTCAGACCGTTAGGCATAGATCTGTGG 29

Db

255 GGCACTCAATTACGAGAAATGCAGAGCCTTGAGGAGCTGATGATTCATATCATATAG 311

101 LeuArgLysGluIleArgArgArgLysGlyGluGluLeuGluGluMetAspIleLysGln 12

DB 315 CTGAGACAGAAATCAGGCGAGAGAGAGGGGCTGAATGATCTTGACATTGCAT 37

Db 375 CTGCGGGCTTTGAGCAATATGACTGAAGCCTTGAATGCTGTGCGTGGCAGGAATAC 433

141 HisValIleLeuAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 16

Db 435 CATGTGATCAAAACACAAAACGAACCTACAGAGAAAGGTGAAGAAITTAGAGGAGAGA 4

DY 161 T Y A R G A I A E u l i e n h s g l u t e u a s p m e t l y s g l u c i n g l u t a s p r o a s n t y g l y 178  
::: :::  
Dh 495 C A T G G A A A C C T T T G A C G G A A T A T G A C A A A A C T A G A G A A T C A C A G A T G T 548

RESULT 13

LOCUS	CA732396	605 bp	mRNA	linear	EST 26-NOV-2
DEFINITION	wip1c.pk005.m21 wip1c	Triticum aestivum	cDNA clone	wip1c.pk005.m	

5' end, mRNA sequence.  
 CA732396  
 CA732396 1 C1-25547994  
 VERBORN

VERSION	01.2023/003
KEYWORDS	CR/2023/01
SOURCE	EST.
	Triticum aestivum (bread wheat)

ORGANISM  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE  
1. (pages 1 to 605)  
Pooideae; Triticeae; Triticum.  
Wolffers D  
Najnov C  
Vujan Z  
Moljan M

TITLE	AUTHORS
Dupont Wheat cDNA Sequence	Dupont, M., Hanafey, M. K., Lingey, S. V., Powell, M., Moltis, F., Miao, G., Caraher, N. and Hanafey, M. K.

**JOURNAL** Unpublished (2002)  
**COMMENT** Contact: Scott V. Tingey  
Cron Genetics

Group Corporation  
E. I. DuPont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

**Tel:** 302-631-2602  
**Fax:** 302-631-2607  
**Email:** [Scott.V.Tingey@usa.dupont.com](mailto:Scott.V.Tingey@usa.dupont.com)

Seq primer: M13.	Location/Qualifiers
1	605

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/organism="Triticum aestivum"
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/db xref="taxon:4565"
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XhoI; Wheat (Triticum aestivum, H1 line) lemma and palea"

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## ORIGIN

## Alignment Scores:

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US-10-690-246A-2 (1-227) x CA732396 (1-605)

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QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyValLeuAlaAspTyrCysSerPro 60
DB 234 GCCCAGGTCCGCATCATCATGTTCTCTCCACCGCGCAAGTACCAAGGTTCTCGAGACC 293
QY 61 SerThrAspIleLeuGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr 80
DB 294 GGCACGACATCAAGGGGATCTTTGACCGCTACCAAGCGCCATCGGAGCACCGCTGTGG 353
QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuValIleValAsnGlnIleAsnGln 100
DB 354 ATGCAGACAGTATAGAAATATGACAGCGCAGCTGAGCATCTCAAGACATCAATCGGAAC 413
QY 101 LeuArgLysGluIleArgArgValGlyGluGluLeuGluGluMetAspIleValGln 120
DB 414 CTGCGCACCGAGATCGAGCAAGAGATGGTGAAGATCTGACCGCTCGAGTTCGAGGAG 473
QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140
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QY 141 HisValIleAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160
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QY 161 TyrArgAlaLeu 164
DB 594 TACAAAGAAATCTN 605

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## RESULT 14

CB972246

692 bp mRNA linear EST 30-APR-2003

CAB10006\_Ia\_Fa\_D07 Cabernet Sauvignon Flower Pre-bloom - CAB1 vitis

vitiifera cDNA clone CAB10006\_Ia\_Fa\_D07 5', mRNA sequence.

CB972246

CB972246.1 GI:30256403

EST

vitis vitiifera

vitis vitiifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; Vitaceae; Vitis.

1 (bases 1 to 692)

Jones da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J.,

Jones,K. and Cook,D.

Expressed sequence tags from Vitis vitiifera 'Cabernet sauvignon'

berries at various developmental stages

## JOURNAL

Unpublished (2003)

Contact: Douglas Cook, PhD

CABs Genome Facility

UC Davis, Plant Pathology

One Shields Ave, Davis, CA 95616, USA

Tel: 530 754 6561

Fax: 530 754 6617

Email: drcook@ucdavis.edu

Seq primer: ACGTACCGACATATGCC.

Location/Qualifiers

## FEATURES

## source

1..692

/organism="Vitis vitiifera"

/mol\_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db\_xref="taxon:29760"

/clone="CAB10006\_Ia\_Fa\_D07"

/sex="Hermaphrodite"

/dev\_stage="Pre-bloom"

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/clone\_lib="Cabernet Sauvignon Flower Pre-bloom - CAB1"

/note="Organ: Flower - Pre-bloom; Vector: pDNR; Site\_1:

SfiI; Site\_2: SfiI; CAB1 is a cDNA library of Vitis

vitiifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples

were collected approximately eleven days before onset of

bloom (clusters at this stage were fully developed and

flowers with calyptres or caps still attached. Sampled

vines were located at the University of California Davis,

Experimental Vineyard. cDNAs were made by oligo-dT priming

and directionally cloned. 5' and 3' adaptors were used in

cloning as follows:

5'-AAGCATGCTATCAACGAGTGGCCATTACGCGCG-3' and

5'-ATTCTAGAGCGGAGCGCGGCGCATG-dT(30)NN-3'. Library was

constructed using the Clontech Creator SMART kit and

size-selected to contain the 0.5-3 kb size fraction."

## ORIGIN

## Alignment Scores:

Pred. No.:	1.47e-55	Length:	692
Score:	556.50	Matches:	112
Percent Similarity:	70.42%	Conservative:	38
Best Local Similarity:	52.58%	Mismatches:	60
Query Match:	47.28%	Indels:	3
DB:	6	Gaps:	3

US-10-690-246A-2 (1-227) x CB972246 (1-692)

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DB 111 TACTCCAAAGCGCGGTCCGGGATCATGAAGAAGCGCGGAGCTCACCGTCTCGGAC 170
QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyValLeuAlaAspTyrCysSerPro 60
DB 171 GCTAAGTTTCTATCATCATGCTCTCCAGTATGAGAAAGCTCCAGTAATCAATGAGCTT 230
QY 61 SerThrAspIleLeuGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTyr 80
DB 231 TCCACTACAACGAACAAATATTGTGATGATCGACGAACACTCTAGAGATGATCATG 290
QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuValIleValAsnGlnIleAsnGln 100
DB 291 AGCTATCACTATGAGAGATGCAAGAAACCTGAAGAAACTGAAGATGAAACAAGAT 350
QY 101 LeuArgLysGluIleArgArgValGlyGluGluLeuGluGluMetAspIleValGln 120
DB 351 CTGAGAAAGAGATTTGGCAGAGCATGGTGAACCTTGAAGCATTTGAGCGCTTGAGAA 410
QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140
DB 411 CTGCGGATCTTGAACAAAGATGAGAGAGTCTTTGAAGATGTTCTGATAGAAATGATAC 470

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: October 6, 2005, 12:46:31 ; Search time 187 Seconds  
(without alignments)  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	611	51.9	946	3	US-09-410-464-2
3	496	42.1	989	4	US-09-640-211A-10
4	357.5	30.4	4285	3	US-09-410-464-1
5	354	30.1	905	4	US-09-640-211A-1944
6	344	29.2	386	4	US-09-640-211A-2008
7	341.5	29.0	779	1	US-08-592-214A-9
8	341.5	29.0	779	3	US-08-655-227-9
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11	341.5	29.0	779	3	US-09-149-976-9
12	341.5	29.0	779	3	US-09-398-326-9

13	341.5	29.0	779	4	US-09-853-450-9	Sequence 9, Appl1
14	326.5	27.7	409	4	US-09-640-211A-1512	Sequence 1512, Ap
15	323	27.4	756	1	US-08-592-214A-11	Sequence 11, Appl
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17	323	27.4	756	3	US-08-655-227-11	Sequence 11, Appl
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22	322.5	27.4	1159	3	US-09-410-464-14	Sequence 14, Appl
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30	320	27.2	756	4	US-08-653-450-13	Sequence 7, Appl1
31	320	27.2	1345	1	US-08-592-214A-7	Sequence 7, Appl1
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38	318	27.0	747	4	US-08-867-087B-12	Sequence 12, Appl
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Sequence 3, Appl1 Application US/09410464  
Patent No. 6395892  
GENERAL INFORMATION:  
APPLICANT: Straube et al.  
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
FILE REFERENCE: 53375  
CURRENT APPLICATION NUMBER: US/09/410,464  
EARLIER FILING DATE: 1999-10-01  
EARLIER APPLICATION NUMBER: 09/287,700  
EARLIER FILING DATE: 1999-04-06  
EARLIER APPLICATION NUMBER: 60/080,851  
EARLIER FILING DATE: 1998-04-06  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 3  
LENGTH: 681  
TYPE: DNA  
ORGANISM: Populus balsamifera subsp. trichocarpa  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (1)..(681)  
US-09-410-464-3

Alignment Scores:  
Pred. No.: 5.73e-71  
Score: 611.00  
Percent Similarity: 70.69%  
Best Local Similarity: 51.17%  
Query Match: 51.91%  
DB: 3  
Gaps: 4  
US-10-690-246A-2 (1-227) x US-09-410-464-3 (1-681)

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; Sequence 2, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; TITLE OF INVENTION: Poplar and other plant species.
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
; US-09-410-464-2

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Query Match: 51.91% Indels: 12
DB: 3 Gaps: 4

US-10-690-246a-2 (1-227) x US-09-410-464-2 (1-946)
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Qy 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerPro 60
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Qy 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsn 100
Db 241 GGCACCTCAATACGAGAAATGCAAGACACCTGAGAACCTGAATGATATCAATCAATAG 300
Qy 101 LeuArgLysGluIleArgArgArgLysGluGluGluLeuGluGluMetAspIleLysGln 120
Db 301 CTGAGACAAAGAAATCAGACAGAGAGAGAGGCGCTGAATGATCTGACATTCATCAT 360
Qy 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValAlaArgHisArgLysTyr 140
Db 361 CTGGCGGCTCTTGAAGCAACATATGACAGAACCTTGAATGATGCTGCGCAGAGAAATAC 420
Qy 141 HisValIleAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160
Db 421 CATGTGATCAAAACACAAACGAAACCTACAGAGAAAGTGAAGATTTTGAAGAGAGA 480
Qy 161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluGluAsnProAsnTyrGlyPheAsn 180
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Qy 215 LeuGlyLeuGlyTyrGluSerHisAspLeuSerLeu 226
Db 643 CTGGAGATGATTTGGAGCCCATGAATCTGCCTT 678

RESULT 3
US-09-640-211A-10
; Sequence 10, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Modifications and Methods for the
; TITLE OF INVENTION: Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16

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Qy      129  luGlusertleuArgIleValArgH1sArgLys 139
Db      2721 CTGAAGCTTGAATGATGCTGCGGACGAGAG 2752

RESULT 5
US-09-640-211A-1944
/ Sequence 1944, Application US/09640211A
/ Patent No. 6833446
/ GENERAL INFORMATION:
/ APPLICANT: Wood, Marion
/ APPLICANT: Shenk, Michael A.
/ APPLICANT: McGrath, Annette
/ APPLICANT: Glenn, Matthew
/ TITLE OF INVENTION: Compositions and Methods for the
/ TITLE OF INVENTION: Modifications of Gene Transcription
/ FILE REFERENCE: 11000.1021CIU
/ CURRENT APPLICATION NUMBER: US/09/640,211A
/ CURRENT FILING DATE: 2000-08-16
/ NUMBER OF SEQ ID NOS: 2368
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1944
/ LENGTH: 905
/ TYPE: DNA
/ ORGANISM: Eucalyptus grandis
US-09-640-211A-1944

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US-10-690-246a-2 (1-227) x US-09-640-211A-1944 (1-905)
Qy      41  AlaGlnValSerIleuMetPheSerSerThrglyLysLeuAlaAspTyrCysSerPro 60
Db      9  TCCCAATCTTCATCATCATCATATCTCCAGCACCGGCAAGCTCCACGAGTACATCAGCCCC 68
Qy      61  SerThraSpIleLysGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp 80
Db      69  TCCACCTCAACGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 128
Qy      81  AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysIleLeuAsnGluIleAsnGlnAsn 100
Db      129  AGCTCTCATATGAGAGATGCAAGAGAACCTGAGAGCTGAGAGAGGTGAACAGAG 188
Qy      101  LeuArgLysGluIleArgTargLysGlyGluGluLeuGluGlyMetAspIleLysGln 120
Db      189  CTTACAGCTGAGAGTCAGAGAGAGGTTCCGGGAGAGATGAAATGATGATGATGATGATG 248
Qy      121  LeuArgLysLeuGluGlnThrLeuGluGluSerLeuArgIleValArgH1sArgLysTyr 140
Db      249  TTGGCGGCTCTTGGCAAGATATGACACAGCCCTTACCTGATCCCTGAAACGAGATAC 308
Qy      141  HisValIleAlaThrGlnThrAspThrTyrIleLysIleLeuLysSerThrArgGluThr 160
Db      309  AAGAGCTCGGCAATCAATGACACCGCCAGGAAGAAAGAAATGCTGAGGAATA 368
Qy      161  TyrArgAlaLeuIleHisGlu-----LeuAspMetLysGluGluAsnPro 175
Db      369  AACAAAGTCTCTCCGCAAGACTGACCAATCTGATCAAGATCTGAGGAGAGAGACCCG 428
Qy      176  AsnTyrGlyPheAsnValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetVal 195
Db      429  CACTTCGGAATG---GTGCAACAC---GGCAGGAGATTACGAGGCTGTGATCGGATATACA 482
Qy      196  Asn-----GluCysProGlnMetPheSerPheArgValValHisProAsnGlnProAsn 213
Db      483  GACGCCGCCGCCGCCGCTGCTGTATACACCTGCGC---CTGCAACCGGACCAAGCCCAAT 539
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Qy      214  LeuLeu---GlyLeuGlyTyrGluSerHisAspLeuSerLeuAla 227
Db      540  CTTACTACGCGGAGAGAGATCGGAGAT-CACGACCTTACCTTGTCT 583

RESULT 6
US-09-640-211A-2008
/ Sequence 2008, Application US/09640211A
/ Patent No. 6833446
/ GENERAL INFORMATION:
/ APPLICANT: Wood, Marion
/ APPLICANT: Shenk, Michael A.
/ APPLICANT: McGrath, Annette
/ APPLICANT: Glenn, Matthew
/ TITLE OF INVENTION: Compositions and Methods for the
/ TITLE OF INVENTION: Modifications of Gene Transcription
/ FILE REFERENCE: 11000.1021CIU
/ CURRENT APPLICATION NUMBER: US/09/640,211A
/ CURRENT FILING DATE: 2000-08-16
/ NUMBER OF SEQ ID NOS: 2368
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2008
/ LENGTH: 386
/ TYPE: DNA
/ ORGANISM: Eucalyptus grandis
US-09-640-211A-2008

Alignment Scores:
Pred. No.:      4.41e-36      Length:      386
Score:          344.00      Matches:      67
Percent Similarity: 74.77%      Conservative: 13
Best Local Similarity: 62.62%      Mismatches: 27
Query Match:    29.23%      Indels:      0
                        Gaps:      0

US-10-690-246a-2 (1-227) x US-09-640-211A-2008 (1-386)
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Db      61  ATGGGTAGAGGGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
Qy      21  TyrSerLysArgArgValGlyIleLeuLysLysValLysGluLeuThrValLeuLysAsp 40
Db      121  TACTCAGACGAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
Qy      41  AlaGlnValSerIleuMetPheSerSerThrglyLysLeuAlaAspTyrCysSerPro 60
Db      181  GCTAGGTTTTCATCTCTCATGCTCTCCGCAACAGAGCTCCAGAGTACATCAGCCCC 240
Qy      61  SerThraSpIleLysGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp 80
Db      241  ACCACACAGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Qy      81  AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysIleLeuAsnGluIleAsnGlnAsn 100
Db      301  ACTACACACTACGATGAAATGCAAGAGAGTTGAGAGAACTGAGAGGTTAATAACAT 360
Qy      101  LeuArgLysGluIleArgArg 107
Db      361  TTTCGAGAGAAATTAAGGACG 381

RESULT 7
US-08-592-214A-9
/ Sequence 9, Application US/08592214A
/ Patent No. 5811536
/ GENERAL INFORMATION:
/ APPLICANT: Yanofsky, Martin F.
/ TITLE OF INVENTION: Cauliflower Floral Meristem Identity
/ TITLE OF INVENTION: Genes and Methods of Using Same
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Campbell and Flores
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
```





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; NAME/KEY: unsure
; LOCATION: 778..779
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..779
; OTHER INFORMATION: /note= "product = Arabidopsis
; OTHER INFORMATION: thaliana CAL."
US-08-655-188-9

Alignment Scores:
Pred. No.: 2.84e-35 Length: 779
Score: 341.50 Matches: 91
Percent Similarity: 54.13% Conservative: 40
Best Local Similarity: 37.60% Mismatches: 80
Query Match: 29.01% Indels: 31
Gaps: 9

US-10-690-246a-2 (1-227) x US-08-655-188-9 (1-779)
QY 1 MetGlyArgGlyLysIleGluIleLysIleGluAsnProThrAsnArgGlnValThr 20
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Db 10 ATGGGAAGGGGTAGGGTTGAATTGAGAGATGAGAAACAAGTCAATAGACAAGTGACA 69
QY 21 TyrSerLysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCyAsp 40
   |||||
Db 70 TTCTCGAAAAGAAAGAACTGGTCTTTTGAAGAACTCGAAGATCTGTTCTTTTGAT 129
QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaSerPro 60
   |||||
Db 130 GCGAGAGTTTCCCTTATGTTCTTCTCCATAGGGAATGTTGAGTACTCTCTGAA 189
QY 61 SerThrAspIleLysGlyIle-----TyrGluArgTyrGlnVal----- 73
   |||||
Db 190 TCTTGATGAGAAAGGTACTAGAAACGTACGAGAGGTATTCTTACGCCGAGACAGCTG 249
QY 74 -----ValThrGlyMetAspLeuThrAsnAlaGlnTyrGluArgMet 87
   |||||
Db 250 ATGGACCTGACTCTACGTTAATGACACAGACAGAACTGGTCTCATGAGGATAGCAGGCTT 309
QY 88 GlnAsnThrLeuLysIleLeuAsnGluIleAsnGlnAsnLeuArgLysGluIleArgArg 107
   |||||
Db 310 AAGGCCAAGATTGAG---CTTTTGAGAGAAACCA-----AGGCAT 348
QY 108 ArgLysGluGluGluLeuGluGluMetAspIleLysGlnLeuArgGlyLeuGluGlnThr 127
   |||||
Db 349 TATCTGGAGAGAAAGTTGGAACCAATGAGCTCAAGATCTCCAAATCTGGAGACAGAC 408
QY 128 LeuGluLeuSerLeuValGlnValArgHisArgLysTyrHisValIleAlaThrGlnThr 147
   |||||
Db 409 CTGAGAGCTGCTCTTAAGACATTCGCTCCAGAAAAAATCAATCAATGAAATGATGATCCCTC 468
QY 148 AspThrTyrLysLysLysLeuLysSerThrArgGluThrTyrArgAlaLeuIleGln 167
   |||||
Db 469 AACCACTCCAAAGAAAGAGAGATACAGAGAGAAACAGACGTTTACCAAGACAG 528
QY 168 LeuAspMetLysGluGluAsnProAsnTyrGlyPheAsnValGluAsnGlnSerArgIle 187
   |||||
Db 529 ATA-----AAGGAGAGGAGAAACATCTTAAGACAAACCAATCATGAGACAG 579
QY 188 TyrGluAsnSerIleProMetValAsnGluCySerProGlnMetPheSer----- 203
   |||||
Db 580 CTGAACCGCAGCGTGACGATGTACACAG---CCACACCATTTTCAACACCCCATCTT 636
QY 204 PheArgValAlaHisProAsnGlnPro-----AsnLeuGluGlyLeuGluTyrGluSer 221
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Db 637 TACATGATCGCTCATCAGACTTCTCTTCTTAATATGGTGGTTTG---TACCAAGA 693
QY 222 HisAsp 223
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Db 694 GAAGAC 699

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RESULT 9
US-08-655-227-9
; Sequence 9, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APETALA1 Gene
; TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,227
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: P-UD 2143
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 779 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..775
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 778..779
; OTHER INFORMATION: /note= "N = one or more
; OTHER INFORMATION: nucleotides."
; NAME/KEY: misc.feature
; LOCATION: 1..779
; OTHER INFORMATION: /note= "product = Arabidopsis
; OTHER INFORMATION: thaliana CAL."
US-08-655-227-9

Alignment Scores:
Pred. No.: 2.84e-35 Length: 779
Score: 341.50 Matches: 91
Percent Similarity: 54.13% Conservative: 40
Best Local Similarity: 37.60% Mismatches: 80
Query Match: 29.01% Indels: 31
Gaps: 9

US-10-690-246a-2 (1-227) x US-08-655-227-9 (1-779)
QY 1 MetGlyArgGlyLysIleGluIleLysIleGluAsnProThrAsnArgGlnValThr 20
   |||||
Db 10 ATGGGAAGGGGTAGGGTTGAATTGAGAGATGAGAAACAAGTCAATAGACAAGTGACA 69
QY 21 TyrSerLysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCyAsp 40
   |||||
Db 70 TTCTCGAAAAGAAAGAACTGGTCTTTTGAAGAACTCGAAGATCTGTTCTTTTGAT 129
QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaSerPro 60

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Db      130 GCCGAGGTTTCCTTAATGTCTTCTCCATTAAGGCAAAATTGTCGAGTACTCTCTGAA
Qy      61 SerThcAsp1IeYsg1Ylle-----TyrGluArgTyrGlnVal-----73
Db      190 TCTTGATGAGAAAGGTACTAGAAAGCGTACGAGAGATTTCTTAAGCCGAGAGACAGCTG
Qy      74 -----ValThrGlyMetAspLeuTPdAmalaglnTyrGluArgMet 87
Db      250 ATTGCACCTGACTCTCACCTTAATGACACAGACGAACTGGTCAATGAGAGATTAGACAGCTT
Qy      88 GlnAsnThrLeuYshIstLeuAnnglnIleAnnglnAnleuArgYsgIleArgArg 107
Db      310 AAGGCCAAGATTGAG--CTTTTGGAGAGAAACCAA-----AGGCAT 348
Qy      108 ArgYsgIYglUglUleuNgIuglUglUleuMetAsp1IeYsg1InLeuArgYglUglUlnThr 127
Db      349 TATCTGGAGAGAAAGATTGAGAACCAATGACCTCAAGAGATCTCCAAAAATCTGAGACAGAG
Qy      128 LeuGluGlnSerLeuArgIleValArgHisArgYsTyrHisValIleAlaThrGlnThr 147
Db      409 CTTGAGAGCTGCTCTTAAGCACATTCGCTCCAGAAAAATTCAACTCATGAAATGAGTCCCTC
Qy      148 AspThrTyrIlybYsYsLeuYsSerThrArgIuTnTyrArgAlaIleuIleGlu 167
Db      469 AACCACTCCAAAGAAAGAGAGAGATACAGAGAGAAACAGACATCTTAACCAACAG
Qy      168 LeuAspMetYsgIuglUlnAnProAntYrGlyPheAsnValGluAnnglnSerArgIle 187
Db      529 ATA-----AAGAGAGAGGAGAAACATCTTAAGACAAACAAACCAATGTAGAGAG
Qy      529 TyrGluAnSerIleProMetValAnngIuYsProGlnMetPheSer-----203
Db      580 CTGAACGCGCGCTCGACAGATGACCAAG--CCACAACCAATTCACACCCCCATCTT
Qy      204 PheArgValValHisProAnngInPro-----AnleuLeuGlyLeuGlyTyrGlnSer 221
Db      637 TACATGATCCCTCATCAGACTTCTCTTCTTAATATGAGTGATTTG--TACCAAGGA
Qy      222 HisAsp 223
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RESULT 10
US-08-655-241-9
: Sequence 9, Application US/08655241
: Patent No. 6025543
: GENERAL INFORMATION:
: APPLICANT: Yanofsky, Martin F.
: APPLICANT: Weisgel, Detlef
: TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
: TITLE OF INVENTION: Development and Methods of Making Same
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell and Flores
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/655,241
: FILING DATE: 05-JUN-1996
: CLASSIFICATION: CLASS 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-UD 1894

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 779 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 10..775
FEATURE:
NAME/KEY: unsure
LOCATION: 778..779
OTHER INFORMATION: /note= "N = one or more
OTHER INFORMATION: nucleotides."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..779
OTHER INFORMATION: /note= "product = Arabidopsis
OTHER INFORMATION: thaliana CAL."
US-08-655-241-9
Alignment Scores:
Pred. No.: 2,84e-35 Length: 779
Score: 341.50 Matches: 91
Percent Similarity: 54.13% Conservative: 40
Best local Similarity: 37.60% Mismatches: 80
Query Match: 29.01% Indels: 31
DB: 3 Gaps: 9
US-10-690-246A-2 (1-227) x US-08-655-241-9 (1-779)
QY 1 MetG|AArgG|LYAs|IleG|Ileu|Ileu|ys|IleG|Ileu|enP|roThr|Aen|Arg|In|Val|Thr 20
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QY 21 TyTser|yA|Arg|Val|G|I|y|Ile|u|ys|I|y|s|a|I|y|s|I|u|e|u|th|r|Val|I|e|u|Cy|Asp 40
Db 70 TTCTCGAAAGAAAGAACTGCTCTTTTGAAGAAAGCTCAGAGATCTGCTCTTTGGAT 129
QY 41 AlG|In|Val|ser|Ile|u|Met|he|ser|Thr|G|I|y|I|s|e|u|A|I|Asp|Ty|Cy|Ser|Pro 60
Db 130 GCCGAGGTTCCCTTATTTGCTCTTCCATAGAGGCAATTTGTCGAGTACTCTCTGAA 189
QY 61 Ser|Thr|Asp|Ile|ys|Ile|-----|Ty|G|I|u|A|r|G|I|Val|----- 73
Db 190 TCTTGCATGAGAAAGGTACTATAGACGCTTACAGAGGTATTCTTACGCCGAGAGACACTG 249
QY 74 -----|Val|Thr|G|I|u|Met|Asp|Leu|TP|Aen|I|Ag|In|Ty|G|I|u|A|r|G|Met 87
Db 250 ATTGCACCTGCACCTCAGCTTATATGACAGACAGAACTGTCATATGAGATATAGCAGGCTT 309
QY 88 Gl|n|Asn|Thr|Ile|u|ys|I|s|e|u|enG|I|I|e|a|enG|I|n|Asn|Leu|A|r|G|I|I|e|A|r|G 107
Db 310 AAGCCCAAAATTAG--CTTTTGGAGAAACCA-----AGGCAT 346
QY 108 Arg|y|s|G|I|u|I|e|u|enG|I|u|enG|I|u|Met|Asp|I|e|ys|I|n|e|u|A|r|G|I|y|I|e|u|G|I|n|Thr 127
Db 349 TATCTGGAGAAAGATTGGAACCAATAGACCTTCAGAGATCTTCCAAAATCTGGACACAG 406
QY 128 Leu|G|I|u|I|e|u|en|Asp|I|e|Val|A|r|G|I|s|A|r|G|I|y|I|s|I|e|A|I|e|A|Thr|G|I|n|Thr 147
Db 409 CTTGAGAGCTGCTCTTAAAGACATGTCCTCCAGAAAATAATCAATCATGATGATGAGTCCCTC 466
QY 148 Asp|Thr|Ty|I|s|y|I|e|u|ys|I|e|u|ys|Ser|Thr|A|r|G|I|u|n|Thr|Ty|A|G|A|I|e|u|I|e|I|s|G|I|u 167
Db 469 AACCACTCCAAAGAAAGAGAGATATCGAGGAGAAAAACAGCATGCTTATCCAAACAG 528
QY 168 Leu|Asp|Met|y|s|G|I|u|I|e|u|enP|ro|Aen|Ty|G|I|y|P|he|Aen|Val|G|I|u|enG|I|n|Ser|A|r|G|I|e 187

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Db 529 ATA-----AAGGAGAGGAAAAACATCTTAAGACAAACCAATGTGACAG 579  
Qy 188 TyGluAnSerIleProMetValAenGluCyBProGImetPheSer-----203  
Db 580 CTGAACCGGCGCTCGACGATGTACACAG---CCACAAACATTTCACACCCCATCTT 636  
Qy 204 PheArgValAlHisProAenGlnPro-----AsnLeuLeuGlyLeuGlyTyrgLuser 221  
Db 637 TACATGATCCCTCATCAGACTTCTCTTCTTAATATGGGTGTTG---TACCAAGA 693  
Qy 222 HisAsp 223  
Db 694 GAAGAC 699  
RESULT 11  
US-09-149-976-9  
Sequence 9, Application US/09149976  
Patent No. 6127123  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Cauliflower Floral Meristem Identity  
TITLE OF INVENTION: Genes and Methods of Using Same  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/149,976  
FILING DATE: 09-SEP-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/592,214  
FILING DATE: 26-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 3291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 779 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 10..775  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 778..779  
OTHER INFORMATION: /note= "N = one or more  
OTHER INFORMATION: nucleotides."  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1  
OTHER INFORMATION: /note= "product = Arabidopsis  
OTHER INFORMATION: thaliana CAL"  
US-09-149-976-9  
Alignment Scores:  
Pred. No.: 2.84e-35 Length: 779

Score: 341.50 Matches: 91  
Percent Similarity: 54.13% Conservative: 40  
Best Local Similarity: 37.60%  
Query Match: 29.01% Indels: 31  
DB: 3 Gaps: 9  
US-10-690-246a-2 (1-227) x US-09-149-976-9 (1-779)  
Qy 1 MetGlyArgGlyLysIleGluIleLysLysIleGluAenProThrAsnArgGlnValThr 20  
Db 10 ATGGGAAGGGGTAGGGTGAATTTGAAGAGATGAGAACAGATCAATGACAGAGACA 69  
Qy 21 TySerLysArgArgValGlyIleLeuLysLysValLysGluLeuThrValLeuCyAsp 40  
Db 70 TTCTGAAAAGAAAGAACTGCTTTTGAAGAAAGCTCAGAGATCTCTTGTGTAT 129  
Qy 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrcysSerPro 60  
Db 130 GCCAGGTTCCCTTATTTGCTTCTCCCATAGGCGCAATTTGAGACTCTCTGAA 189  
Qy 61 SerThrAspIleLysGlyIle-----TyrgLysTyrgLysVal-----73  
Db 190 TCTTGATGAGAGAGTACTTACAGCGCTAGAGAGATTTCTTACGCCGAGACACTG 249  
Qy 74 -----ValThrGlyMetAspLeuThrAsnAlaGlnTyrgLysMet 87  
Db 250 ATTGCACCTGACTCTACGCTTAATGACAGAGAACTGGTCAATGAGATGACAGGCTT 309  
Qy 88 GlnAenThrLeuLysLeuAenGluIleAenGlnAenLeuArgLysGluIleArgArg 107  
Db 310 AAGGCCAAGATTGAG---CTTTTGGAGAAACCA-----AGGCAT 348  
Qy 108 ArgLysGlyGluGluLeuGluIleLysMetAspIleLysGlnLeuArgGlyLeuGluGlnThr 127  
Db 349 TATCTGGAGAAAGATGGAACCAATGACCTCAAGATCTCAAAATTTGAGACAGCAG 408  
Qy 128 LeuGluGluSerLeuArgLysValArgHisArgLysTyrgLysValIleAthrGlnThr 147  
Db 409 CTTGAGACGCTCTTAAGCACTTGGCTCCCAAAAAATCAACTGATGAATGAGCCCTC 468  
Qy 148 AspThrTyrgLysLysLeuLysSerThrArgGluThrTyrgAlaLeuIleHisGlu 167  
Db 469 AACCACTCCAAAGAAAGAGAGATACAGGAGAAACAGCATGCTTCCAAACAG 528  
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Qy 188 TyGluAnSerIleProMetValAenGluCyBProGImetPheSer-----203  
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Qy 222 HisAsp 223  
Db 694 GAAGAC 699  
RESULT 12  
US-09-398-326-9  
Sequence 9, Application US/09398326  
Patent No. 6355863  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Campbell and Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego

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STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 779 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 10..775
FEATURE:
NAME/KEY: unsure
LOCATION: 778..779
OTHER INFORMATION: /note= "N = one or more
OTHER INFORMATION: nucleotides."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..779
OTHER INFORMATION: /note= "product = Arabidopsis
OTHER INFORMATION: thaliana CAL."
US-09-398-326-9

Alignment Scores:
Pred. No.: 2,84e-35 Length: 779
Score: 341.50 Matches: 91
Percent Similarity: 54.13% Conservative: 40
Best Local Similarity: 37.60% Mismatches: 80
Query Match: 29.01% Indels: 31
Gaps: 9
DB: 3

US-10-690-246a-2 (1-227) x US-09-398-326-9 (1-779)
QY 1 MetGlyArgGlyIleGluIleGlyIleGluAsnProThrAsnArgGlnValThr 20
DB 10 ATGGGAAGGGGTAGGTTGAATTGAAAGATAGAGAAACAATGATCAATAGCAAGTGACA 69
QY 21 TySerIleYsaArgValGlyIleLeuIleYsaIalYsgIuLeuThrValLeuCyasp 40
DB 70 TTCTCGAAMAGAAAGATGCTCTTTTGAAGAAAGCTCAGGAGATCTCTGTTCTTGTGAT 129
QY 41 AlaGlnValSerIleuIleMetPheSerSerThrGlyIleuAlaAspTyCySerPro 60
DB 130 GCCAAGTTTCCCTTATGTCCTCTCCCATTAAGGCAATGTTGCAATGCTCCTCTGAA 189
QY 61 SerThrAspIleYsgIle-----TyrgIuArgTyrgIuVal----- 73
DB 190 TCTTGCAATGAGAAAGGTACTAGAACGCTACGAGAGTATCTTACGCCGAGACAGCTG 249
QY 74 -----ValThrGlyMetAspLeuTPanAlaGlnTyrgIuArgMet 87
DB 250 ATTGCACCTGACTCTCAGGTTAATGACAGACGAACTGTCTCATGAGATATGCAAGCTT 309

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QY 88 GlnAsnThrLeuIleYshIleuAsnGluIleAsnGlnAsnLeuArgYsgIuIleArg 107
DB 310 AAGGCCAAGATTGAG---CTTTGGAGAGAAACCA-----AGGCAT 348
QY 108 ArgYleGlyGluGluLeuGluGluIleMetAspIleYsgIleuArgGlyLeuGluGlnThr 127
DB 349 TATCTGGAGAAAGATTGGAACCAATGAGCCTCAAGACTCCAAATCTGGAGACGAG 408
QY 128 LeuGluGluSerLeuArgIleValAlaArgHisArgYleTyHisValIleAlaThrGlnThr 147
DB 409 CTGAGACTGCTCTTAAGCAATCCCTCCAGAAAAATCAATCAATGATGATGATGCTTC 468
QY 148 AspThrTyIleYsaIleYleuYserThrArgGluThrTyArgAlaLeuIleHisGlu 167
DB 469 ACCACCTCCAAAGAAAGAGAGATACGAGAGAGAAAAACGACATGCTTACCAAAACG 528
QY 168 LeuAspMetIleYsgIuIleAsnProAsnTyrgIlePheAsnValGluAsnGlnSerArgIle 187
DB 529 ATA-----AAGAGAGAGGAAACATCTTAAGACAAACAAACCAATGATGACGAG 579
QY 188 TyrgIuAsnSerIleProMetValaAngIuCyAspGlnMetPheSer----- 203
DB 580 CTGACCGGAGCGCTGACGATGATACCAAG---CCAAACCATTTCAACACACCCCATCTT 636
QY 204 PheArgValValHisProAsnGlnPro-----AsnLeuGluIleuGlyTyrgIuSer 221
DB 637 TACATGATCGCTCATGACATCTCTCTTCTTAATATGAGTGGTGTG---TACCAAGCA 693
QY 222 HisAsp 223
DB 694 GAAAGAC 699

RESULT 13
US-09-853-450-9
Sequence 9, Application US/09853450
Patent No. 6828478
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 779
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURES:
NAME/KEY: CDS
LOCATION: (10)..(777)
OTHER INFORMATION: CAULIFLOWER (CAL)
NAME/KEY: modified base
LOCATION: (778)..(779)
OTHER INFORMATION: n = g, a, c or t
US-09-853-450-9

Alignment Scores:
Pred. No.: 2,84e-35 Length: 779
Score: 341.50 Matches: 91
Percent Similarity: 54.13% Conservative: 40
Best Local Similarity: 37.60% Mismatches: 80
Query Match: 29.01% Indels: 31
Gaps: 9
DB: 4

US-10-690-246a-2 (1-227) x US-09-853-450-9 (1-779)
QY 1 MetGlyArgGlyIleGluIleGlyIleGluAsnProThrAsnArgGlnValThr 20

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Db      10 ATGGAGAGGGGTAGGGTTGAAATTGAAAGAGATGAGAACAGATCATATGACAAAGTGACA 69
Qy      21 TyrSerLeuArgArgValGlyIleLeuLysAlaLysGluLeuThrValLeuCybAap 40
Db      70 TTCTCGAAAAGAAAGAACTGGTCTTTGAAAGAAAGCTCAGAGAGTCTGTTCTTTGTGTAT 129
Qy      41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLeuLeuAlaAspTyrCybSerPro 60
Db      130 GCCGAGGTTTCCTTATTGCTTCTTCTCCCATTAAGGCAAAATGTTTCCAGATCTCTCTGAA 189
Qy      61 SerThrAspIleLysGlyIle-----TyrGluArgTyrGlnVal----- 73
Db      190 TCTTGATGGAGAAAGGACTAGAAACGCTACGAGAGGATATTCTTAAGCCGAGAGACAGCTG 249
Qy      74 -----ValThrGlyMetAspLeuThrAsnAlaGlnTyrGluArgMet 87
Db      250 ATTGCACTGACTCTCAACGTTAATGCAACAGCAACCTGGTCAATGAGTATGACAGGCTT 309
Qy      88 GlnAsnThrLeuLysIleLeuAsnGlnIleAsnGlnAsnLeuArgLysGluIleArgArg 107
Db      310 AAGGCCAAGATTGAG---CTTTGGAGAGAAACCA-----AAGCAT 348
Qy      108 ArgLysGlyGluGluLeuGluGluGlyMetAspIleLysGlnLeuArgLysGluGlnThr 127
Db      349 TATCTGGAGAGAAAGTTGAAACCAATGAGCTCAAGATCTCCAAATCTGGAGACAGCA 408
Qy      128 LeuGluGluSerLeuArgIleValArgHisArgLysTyrHisValIleAlaThrGlnThr 147
Db      409 CTTGAAACCTGCTCTTAAGCAATTCGCTCCAGAAAATACTCAACTCAATGAGTGCCTTC 468
Qy      148 AspThrTyrIleLysLysLeuLysSerThrArgGluThrTyrArgAlaLeuIleHisGlu 167
Db      469 AACCACTCCAAAGAAAGAAAGAGATACAGAGAGAAACAGCATCTTACCAAAACAG 528
Qy      168 LeuAspMetLysGluGluAsnProAsnTyrGlyPheAsnValGluAsnGlnSerArgIle 187
Db      529 ATA-----AAGAGAGAGGAAACATCTCTTAAGCAAAACAAACCCCAATGTGACAG 579
Qy      188 TyrGluAsnSerIleProMetValAsnGluCybProGlnMetPheSer----- 203
Db      580 CTGAAACCGACGCTCGACATGTAACAG---CCACAAACATTTCAACACCCCATCTT 636
Qy      204 PheArgValValHisProAsnGlnPro-----AsnLeuGluGlyLeuGlyTyrGluSer 221
Db      637 TACATGATCGCTATCAGACTTCTCTTCTTAATATGGGTGTTG---TACCAAGCA 653
Qy      222 HisAsp 223
Db      694 GAAGAC 699

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RESULT 14
US-09-640-211A-1512
; Sequence 1512, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640.211A
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1512
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1512

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Alignment Scores:
Pred. No.: 9,89e-34 Length: 409
Score: 326.50 Matches: 70
Percent Similarity: 63.24% Conservative: 16
Best Local Similarity: 51.47% Mismatches: 49
Query Match: 27.74% Indels: 1
DB: 4 Gaps: 1

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US-10-690-246A-2 (1-227) x US-09-640-211A-1512 (1-409)
Qy      7 GluIleLysLysIleGluAsnProThrAsnAlaGlnValThrTyrSerLeuArgArgVal 26
Db      1 GAGAGACAGAAAGAAATTAAGAACAGACAGCAAGGAAAGCTTCTCGAAGCGAGGAAT 60
Qy      27 GlyIleLeuLysAlaLysGluLeuThrValLeuCybAspAlaGlnValSerLeuIle 46
Db      61 GGCATCTCAAGAAAGCCACAGAGCTCACGCTCTCTGCGAGCTTAGGGTTCCATCTTC 120
Qy      47 MetPheSerSerThrGlyLysLeuAlaAspTyrCybSerProSerThrAspIleLysGly 66
Db      121 ATGCTCTCGGAGAACAGAGAGCTCCAGAGTACATCAGCCCAACCAACGACAAAGAG 180
Qy      67 IleTyrGluArgTyrGlnValValThrGlyMetAspLeuThrAsnAlaGlnTyrGluArg 86
Db      181 ATGATTGATGATTACAGAGAGGCTCTGGATCGATCTGTGACTGACTACACACTACATGA 240
Qy      87 MetGlnAsnThrLeuLysIleLeuAsnGlnIleAsnGlnAsnLeuArgLysGluIleArg 106
Db      241 ATGCAAGAGAGAGTTGAGAACTGAAGAGAGTTAATACATTTTCGAGAGAAATTAAG 300
Qy      107 ArgArgLysGlyGluGluLeuGluGluGlyMetAspIleLysGlnLeuArgLysGluGln 126
Db      301 CGATATTGGCCAGCATTTGAACGAGCTGACGCTACGCAAGCTCAGACAGTCCGAGCA 360
Qy      127 ThrLeuGluGluSerLeuArgIle---ValArgHisArgLysTyrHis 141
Db      361 GACGATCCAGATCTTGTCAATTCAGATGCGGAGAAAGAAAGTACCAT 408

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RESULT 15
US-08-592-214A-11
; Sequence 11, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 base pairs

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Search completed: October 6, 2005, 15:22:14  
Job time : 192 secs

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:      TYPE: nucleic acid
:      STRANDEDNESS: double
:      TOPOLOGY: linear
:      MOLECULE TYPE: cDNA
:      FEATURE:
:      NAME/KEY: CDS
:      LOCATION: 1..754
:      FEATURE:
:      NAME/KEY: misc_feature
:      LOCATION: 1..756
:      OTHER INFORMATION: /note= "product = Brassica oleracea
:      OTHER INFORMATION: CAL"
:
US-08-592-214A-11

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 6, 2005, 13:00:26 ; Search time 711 Seconds  
(without alignments)  
2223.655 Million cell updates/sec

Title: US-10-690-246a-2

Perfect score: 1177

Sequence: 1 MGGKIKIKIENPTNRQVT.....HPNQPLGLGYSHDLSTA 227

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 844330 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2\_1/USPTO.spool/US10690246.rnmat 05102005 110912 6499/app.query.fasta\_1.391  
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-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62  
-TRANS=human40.ccd -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
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- 6: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
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- 23: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	802.5	68.2	1036	20	US-10-690-246-5
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4	755	64.1	898	20	US-10-690-246-7
5	675	57.3	681	17	US-10-260-238-5530
6	675	57.3	1257	21	US-10-343-477A-45
7	611	51.9	681	14	US-10-104-580-3
8	611	51.9	946	14	US-10-104-580-2
9	576	48.9	637	21	US-10-487-901-7033
10	557.5	47.4	926	21	US-10-343-477A-49
11	556.5	47.3	1036	18	US-10-424-599-120794
12	529.5	45.0	871	18	US-10-425-114-10670
13	528.5	44.9	644	19	US-10-021-323-8631
14	521.5	43.3	630	21	US-10-487-901-7174
15	509.5	43.3	664	21	US-10-487-901-3483
16	509.5	43.3	665	21	US-10-487-901-7018
17	496	42.1	989	20	US-10-856-499-10
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21	472	40.1	1155	18	US-10-424-599-66649
22	471.5	40.1	1231	18	US-10-425-114-15025
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24	445	37.8	2718	18	US-10-424-599-120795
25	438	37.2	2237	18	US-10-425-114-11390
26	432	36.7	951	19	US-10-767-795-2121
27	427.5	36.3	639	19	US-10-021-323-86882
28	415	35.3	964	20	US-10-739-930-3300
29	414	35.1	425	11	US-09-922-293-14
30	413	35.1	669	19	US-10-021-323-88899
31	413	35.1	1007	18	US-10-425-114-11870
32	413	35.1	1021	18	US-10-424-599-65326
33	412	35.0	607	11	US-09-922-293-3394
34	406	34.0	401	19	US-10-021-323-13542
35	400	34.0	886	15	US-10-278-536-238
36	400	34.0	914	18	US-10-412-699B-55
37	399	33.9	632	21	US-10-487-901-3376
38	397	33.7	742	21	US-10-487-901-3474
39	393	33.4	474	11	US-09-732-627A-4667
40	391.5	33.3	674	21	US-10-487-901-3487
41	386	32.8	401	11	US-09-922-293-13
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44	385	32.7	780	21	US-10-889-684-4
45	382.5	32.5	535	11	US-09-732-627A-3282

#### ALIGNMENTS

RESULT 1  
US-10-690-246-1  
; Publication 1, Application US/10690246  
; Publication No. US20040210967A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEN, HONG-HWA  
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID  
; PTL REFERENCE: U 014863-8  
; CURRENT FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: 091125320  
; PRIOR FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1

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/ LENGTH: 917
/ TYPE: DNA
/ ORGANISM: Phalaenopsis equestris
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (76)..(759)
US-10-690-246-1

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Pred. No.: 2,92e-128 Length: 917
Score: 1177.00 Matches: 227
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-10-690-246a-2 (1-227) x US-10-690-246-1 (1-917)

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QY 21 TyrSerLysArgArgValGlyIleLeuLysLysAlaLysGluLeuThrValLeuCyAsp 40
Db 136 TATTCTTAAGAGAGAGTTGGGATCTGTAAGAGGCCAAGGAGCTACTGTTCTCTGAT 195
QY 41 AlaGlnValSerLeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCySerPro 60
Db 196 GCTCAGGCTCTCTCATCATGATGTTCTCAAGCACAGAAAGTTGGCTGATTAAGAGCC 255
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Db 256 TCTACTGATATTAAAGGGATATATAGAGGATCAAGGTTGATGATGATGATCTATAG 315
QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysIleLeuAsnGluIleAsnGlnAsn 100
Db 316 AATGCTCAGTATAGAGAGATGACAGATACGCTGAGCATCTGAATGATTAACCAAAAC 375
QY 101 LeuArgLysGluIleArgArgArgLysGlyGluIleGluIleGluMetAspIleLysGln 120
Db 376 CTAGAGGAAGGAGATTAGAGAGAGAGAGAGGAGGAGAAATGGAGGCGATGACATTAAGCAA 435
QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140
Db 436 CTGCGCGGCTTTGAGCAAACTTTGGAAGAGTCTCTTGATTTGTTAGGCAATAGAAATAT 495
QY 141 HisValIleAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160
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QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluIleAsnProAsnTyrGlyPheAsn 180
Db 556 TACCGCGCTTAATACATGAACTGATATGAAAGAGAGAAATCCGAACCTACGGTTTAAT 615
QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCySerProGln 200
Db 616 GTGAAAGAACAGAGTAGAATTATGAAATTCGATTCGAATGGGATGATGATGCTCCAG 675
QY 201 MetPheSerPheArgValValHisProAsnGlnProAsnLeuLeuGlyLysGlyTyrGlu 220
Db 676 ATGTTTTCCTTTAGGGGTGTTGATCCGAATCCGAATCAGCCCAATCGCTTGAGTTATGAA 735
QY 221 SerHisAspLeuSerLeuAla 227
Db 736 TCAATGATCTTAGCCTTGCA 756

RESULT 2
US-10-690-246-5
/ Sequence 5, Application US/10690246
/ Publication No. US20040210967A1
/ GENERAL INFORMATION:
/ APPLICANT: CHEN, HONG-HWA
/ APPLICANT: TSAI, WEN-CHIEH
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/ TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
/ FILE REFERENCE: U 014863-8
/ CURRENT APPLICATION NUMBER: US/10/690,246
/ CURRENT FILING DATE: 2003-10-21
/ PRIOR APPLICATION NUMBER: 091125320
/ PRIOR FILING DATE: 2002-10-25
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 5
/ LENGTH: 1036
/ TYPE: DNA
/ ORGANISM: Phalaenopsis equestris
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (216)..(887)
US-10-690-246-5

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Pred. No.: 4,56e-84 Length: 1036
Score: 802.50 Matches: 148
Percent Similarity: 85.90% Conservative: 47
Best Local Similarity: 65.20% Mismatches: 29
Query Match: 68.18% Indels: 3
DB: 20 Gaps: 2

US-10-690-246a-2 (1-227) x US-10-690-246-5 (1-1036)

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QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuLysIleLeuAsnGluIleAsnGlnAsn 100
Db 456 AGCTCCGACTTACGAAAGATGCTGATTAACCTTAACCAATTCGAAGAGATCAATGCAAT 515
QY 101 LeuArgLysGluIleArgArgArgLysGlyGluIleGluIleGluMetAspIleLysGln 120
Db 516 CTGAGGAGGGAAGTAAAGCAGAGAGATGGGGAAGATCTTGAGGAGACTGATATCAAGGAA 575
QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyr 140
Db 576 CTGCGCGGCTTTGAGCAAAACATTTGATGAGGATGGAACCTGATCGAAATAGAAAATAT 635
QY 141 HisValIleAlaThrGlnThrAspThrTyrLysLysLysLeuLysSerThrArgGluThr 160
Db 636 CATGTATACATGATCTAAACGACACCTTCAAGAAAGATTGAAGAACTCCCAAGAAACA 695
QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLysGluIleAsnProAsnTyrGlyPheAsn 180
Db 696 CACCGGAACCTTAATGACGAATTTGGAATCGTTGAGAGCACCAAGTGTATGGGTTCCAC 755
QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCySerProGln 200
Db 756 GAGGATTAAGCAAT-----TATGAGGGGTGTTCTTCTTCAATACCGGCTTCAC 809
QY 201 MetPheSerPheArgValValHisProAsnGlnProAsnLeuLeuGlyLysGlyTyrGlu 220
Db 810 ATGTATGCTTCCG---GTGCAACCCCAACCAAAATCTTCAAGAGAACGGGATTAAC 866
QY 221 SerHisAspLeuSerLeuAla 227
```

Db 867 TCTCAGCATCTTCGCTCGCT 887

RESULT 3  
US-10-690-246-3  
; Sequence 3, Application US/10690246  
; Publication No. US20040210967A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEN, HONG-HWA  
; APPLICANT: TSAI, WEN-CHIEH  
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID  
; FILE REFERENCE: U 014863-8  
; CURRENT APPLICATION NUMBER: US/10/690,246  
; CURRENT FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: 091125320  
; PRIOR FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 980  
; TYPE: DNA  
; ORGANISM: Phalaenopsis equestris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (196)..(864)  
US-10-690-246-3

Alignment Scores:  
Pred. No.: 6.4e-79 Length: 980  
Score: 758.50 Matches: 142  
Percent Similarity: 81.94% Conservative: 44  
Best Local Similarity: 62.56% Mismatches: 36  
Query Match: 64.44% Indels: 5  
DB: 20 Gaps: 2

US-10-690-246A-2 (1-227) x US-10-690-246-3 (1-980)

Qy 1 MetGtAArGgLYlVlellleGluIleLybLySIleGluAsnProThrAsnArgInValThr 20  
Db 196 ATGGGGAAGGGGGAAGATTCAGATTAAGAAGATTGAGAACCCCTACAAACAGGAGTTACT 255  
Qy 21 TTrSerLYsArGArGValSIyleuLYbLYsAlAlaLyGluuThrValleuCYsAsp 40  
Db 256 TACTCTTAAGAGAGAGGCTGTGGATCATGAATAAGGCGAGAGGTCAAGTCTCTGTGAT 315  
Qy 41 AlagInValSerIleuIleMetPheSerSerThrGlyLYleuAlaAspTYrCYsSerPro 60  
Db 316 GGTCAAGCTCTCCCTTGTATGTTCCTCCAGACCGGCAAGTTCGAGATATTGTATGCT 375  
Qy 61 SerThrAspIleLeuSgLYleTYrGluAqTYrGlnValValThrGlyMetAspLeuTrp 80  
Db 376 ACCACCGAATACCAAGAGTGTATGTATGCTTACCACAGAGTGTCCGGCAATAAATTATGG 435  
Qy 81 AanaIaGlnTYrGluArMetGlnAsnThrIleuLYbIleuAsnGlnIleAsnGlnAsn 100  
Db 436 AGGAGACAGTACCAAGAAATGCAAAATACCTTAATCATTTGAAGAGATTAACCAACAC 495  
Qy 101 LeuArGlyeGluIleArGArGArGlySgLYgluGluLeuGluGlyMetAspIleLYgln 120  
Db 496 TTGAGAGAGGAGATTAAGGACAGAGATGGGGGAGAGATCTTGAAGGCTAGAAATCAAGAA 555  
Qy 121 LeuArGlyeGluGluGlnThrIleuGluGlnSerIleuArGlyeValArGhISarGlyeTYr 140  
Db 556 CTGCGGTGCTTGTAGCAAAATATAGACAGAGGCGCTTAAGCTTGAAGAAATCAAAAGTAT 615  
Qy 141 HisValIleAlaArhGlnThrAspTrpTYrLYbLYbLYbLeuLYbSerThrArGluThr 160  
Db 616 CACGTATCATGACCCACAGACAGATCATTTCAAAAAAAAAAGTTGAAAAACTTCAAGAAAC 675  
Qy 161 TYrArGAlaLeuIleHISgIleuAspMetLYsGluGluAsnProAsnTYrGlyPheAsn 180  
Db 676 CACAGAACTTACTCCGGGAGCTG-----GAACTGAGCACCGCGTCTACTAC 723  
Qy 181 ValGluAsnGlnSerArGlyeTYrGluAsnSerIleProMetValaAsnGluCYbProGln 200

Db	724	GGGAGTGTGATGATCCAAACACTGATGATGGCGCGCTTGCACTTGGAAATGGGGCTTCTAC	783
Qy	201	MetPheSerPheArgValValHisProAsnGlnProAsnLeuLeuGlyLeuGlyTyrGlu	220
Db	784	TGTGATTGATTTGCT---ACCAACCAAGCAGCCGCAACCTTCAGGAGAGTGGATATGTC	840
Qy	221	SerHisAspLeuSerLeuVala	227
Db	841	CCTCATGATCTACGTTCTGACC	861
RESULT 4			
US-10-690-246-7			
Sequence 7,	Application US/10690246		
Publication No.	US20040210967A1		
GENERAL INFORMATION:			
APPLICANT:	TSAI, HONG-HWA		
APPLICANT:	CHEN, HONG-CHIEH		
TITLE OF INVENTION:	GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID		
FILE REFERENCE:	U 014863-8		
CURRENT APPLICATION NUMBER:	US/10/690,246		
PRIOR FILING DATE:	2003-10-21		
PRIOR APPLICATION NUMBER:	091125320		
NUMBER OF SEQ ID NOS:	24		
SOFTWARE:	Patentin version 3.2		
SEQ ID NO 7			
LENGTH:	898		
TYPE:	DNA		
ORGANISM:	Phalaenopsis equestris		
FEATURE:			
NAME/KEY:	CDS		
LOCATION:	(123) .. (782)		
US-10-690-246-7			
Alignment Scores:			
Pred. No.:	1,466-78	Length:	898
Score:	755.00	Matches:	149
Percent Similarity:	82.59%	Conservative:	36
Best Local Similarity:	66.52%	Mismatches:	29
Query Match:	64.15%	Indels:	10
DB:	20	Gaps:	2
US-10-690-246A-2 (1-227) x US-10-690-246-7 (1-898)			
Qy	1	MetGlyArgGlyValysileglnlelybysileglnaenProthrAsnArglnValThr	20
Db	123	ATGGGAGAGGAGGAAGTATAGATTAAGAAGATAGAGATCCAAACAGGCAAGTAAACG	182
Qy	21	TyrSerIyehArgArgValGlylleuLybValalysglulnuthrValleuCyAsp	40
Db	183	TATTCAAAGGCGCACTTGGGATCATGAAGAAGCGAGGAACCTCACAGTGCCTTGCGAC	242
Qy	41	AlaGlnValSerleuIleMetPheSerSerThrGlyLySleuAlaAspYrCySerPro	60
Db	243	GCTCAATCTCAGCTCATCTCATCTTCTTCAGCTCCGCAAGTTACGTATCTCGACGCT	302
Qy	61	SerThrAspIlelysglyIleTyrGlyGlnArgGlnValThrGlyMetAspLeuTrp	80
Db	303	TCCACAGACGTTAAAGATATAGTATGAGAGGTACCAAAATGTTACCGGAAATGATATATGG	362
Qy	81	AsnAlaGlnTyrGlyLysMetGlnIleAsnThrIleuLybHisleuAsnGlnIleAsnGlnAsn	100
Db	363	GATCCGCAATATACAGAGATGCGAGAACATCTCGAGGAATCTCAGGAGATTAATCGTAAAT	422
Qy	101	LeuArgIyegIuIleArgArgArgIyegIyGlnIleuGlnIleuGlyMetAspIleysGln	120
Db	423	CTTCAGAGAGAGATTAAGACAGAGGAAGCGGAGGATCTCGAAGGGTTCGGCGTTAAAGAG	482
Qy	121	LeuArgIyegIuGlnIleThrIleuGlnIleuSerIleuArgIleValArgHisArgIyLeuTyr	140
Db	483	CTGGCGGCTCTTGAGCAAAAATTTGGAGGAGTGGTTAAAGATTTGTCGGCAGAGAAAGTAT	542



Best Local Similarity: 58.95% Mismatches: 51  
 Query Match: 57.35% Indels: 6  
 DB: 21 Gaps: 5

US-10-690-246a-2 (1-227) x US-10-343-477A-45 (1-1257)

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QY 1 MetGlyArgGlyValIleGluIleValIleGluAsnProThrAsnArgGlnValThr 20
DB 131 ATGGGGCGCGCAAGATCGAGATCAAGCGGATCGAGAAAGCCCAACCGCCAGGTGACC 190
QY 21 TySerIleArgArgValGlyIleLeuValAlaValSerGluLeuThrValIleuCyasp 40
DB 191 TACTCAAGCGCGGAGCGGAGATCATCAAGAGCGCGCACTCCGCTCTGCGAC 250
QY 41 AlaGlnValSerIleuIleMetPheSerSerThrGlyValLeuAlaAspTyrCySerPro 60
DB 251 GCCAGGTGCGCATCATGTTCTCTCCACCGGCAAGTACACAGAGTTCTGACAGCCC 310
QY 61 SerThrAspIleValSerGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp 80
DB 311 GGAACCGACATCAAGACCATCTTACCGGTACCAAGAGCGCATTCGGACCAAGCTATGG 370
QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrIleuValHisIleuAsnGluIleAsnGlnAsn 100
DB 371 ATGAGCAGATATGAGATATGACCGCAAGCTGAGCCATCTCAAGACATCATCTGCT 430
QY 101 LeuArgIleGluIleArgArgValGlyIleGluIleuGluIleuMetAspIleValSerGln 120
DB 431 CTGGCGCAGAGATTAAGCAAAAGATGGCGAGATCTGGACAGTCTGACCTTGACGAG 490
QY 121 LeuArgIleuGluIleuThrIleuGluIleuSerIleuArgIleValArgHisArgValTyr 140
DB 491 CTGGCGCGCTCGAGCAAAAGCTGACGCGCTCTCAAGAGAGTTCGCCATTAAGAACTAC 550
QY 141 HisValIleAlaThrGlnThrAspThrTyrIleValSerIleuValSerThrArgGluThr 160
DB 551 CATGTGATCAGACGACGACATGATACCTTACAGAAAGAGTGAAGCACTGCGACGAGCG 610
QY 161 TyrArgAlaLeuIleHisGluLeuAspMetIleGluIleuAsnProAsnTyrGlyPheAsn 180
DB 611 TACAGAACTCTGACGAGAGAGCTAGCGATGCGGAGAGC---CCGGGCTTCGGGTAC--- 664
QY 181 ValGluAsnGlnSerArg-----IleTyrGluAsnSerIleProMetValAsnGluCys 198
DB 665 GTGGACAACACGCGCGCGCGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGC 724
QY 199 ---ProGlnMetPheSerPheArgValValHisProAsnGlnProAsnLeuGluIleu 217
DB 725 CCGCGGAGCATGTAGCGCTTCGCGTGGTG---CCAGCGCAAGCCCAACCTGACAGCGCATG 781
QY 218 G1TyrGluSerHisAspLeuSerIleu 226
DB 782 GCCTACGGCTTCCACGACCTCCGCGCTG 808

```

RESULT 7  
 US-10-104-580-3

; Sequence 3, Application US/10104580  
 ; Publication No. US20030033628A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Straus et al.  
 ; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
 ; FILE REFERENCE: 62486  
 ; CURRENT APPLICATION NUMBER: US/10/104,580  
 ; PRIOR APPLICATION NUMBER: 09/410,464  
 ; PRIOR FILING DATE: 1999-10-01  
 ; PRIOR APPLICATION NUMBER: 09/287,700  
 ; PRIOR FILING DATE: 1999-04-06  
 ; PRIOR APPLICATION NUMBER: 60/080,851  
 ; PRIOR FILING DATE: 1998-04-06  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3  
 ; LENGTH: 681  
 ; TYPE: DNA  
 ; ORGANISM: Populus balsamifera subsp. trichocarpa  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(681)  
 US-10-104-580-3

#### Alignment Scores:

Pred. No.:	8,92e-62	Length:	681
Score:	611.00	Matches:	128
Percent Similarity:	70.69%	Conservative:	36
Best Local Similarity:	55.17%	Mismatches:	56
Query Match:	51.91%	Indels:	12
DB:	14	Gaps:	4

US-10-690-246a-2 (1-227) x US-10-104-580-3 (1-681)

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QY 1 MetGlyArgGlyValIleGluIleValIleGluAsnProThrAsnArgGlnValThr 20
DB 1 ATGGGTGCGGAAAGATGAAATCAAGAGATCGAAAGATCCCAACAGCGCAAGTCACC 60
QY 21 TySerIleArgArgValGlyIleLeuValAlaValSerGluLeuThrValIleuCyasp 40
DB 61 TACTCAAGAGAAAGATGATTTTCAAGAAAGCCCAAGAACTCACTGATTTGAT 120
QY 41 AlaGlnValSerIleuIleMetPheSerSerThrGlyValLeuAlaAspTyrCySerPro 60
DB 121 GCTAAGTCTCTTATCATGTTCTCCAACTTACAACTCAATCAATGATTAAGTACCC 180
QY 61 SerThrAspIleValSerGlyIleTyrGluArgTyrGlnValValThrGlyMetAspLeuTrp 80
DB 181 TCCACATTCAGCAAGAAAGATACGATCAATATCAAGACCTTTAGCATAGATCTGTGG 240
QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrIleuValHisIleuAsnGluIleAsnGlnAsn 100
DB 241 GGCATCATATACAGAAAGATGCAAGAGCACTTGAAGAGCTGATATCATATCAATTAAG 300
QY 101 LeuArgIleGluIleArgArgValGlyIleGluIleuGluIleuMetAspIleValSerGln 120
DB 301 CTGAGCAAGAAATTCAGGAGAGAGAGAGAGAGGCGCTGATGATGATGATGATGATCAT 360
QY 121 LeuArgIleuGluIleuThrIleuGluIleuSerIleuArgIleValArgHisArgValTyr 140
DB 361 CTGGCGCGCTTGAAGCAATATGATGAAAGCTTGAAGTGTGTGTGCGTGCAGAGAACTAC 420
QY 141 HisValIleAlaThrGlnThrAspThrTyrIleValSerIleuValSerThrArgGluThr 160
DB 421 CATGTGATCAAAACACAAACGAAACCTTACAGAAAGAGTGAAGATTTAAGAGAGAGA 480
QY 161 TyrArgAlaLeuIleHisGluLeuAspMetIleGluIleuAsnProAsnTyrGlyPheAsn 180
DB 481 CATTGAAACCTCTTGAATGAAATGAAAGCAAAACTGAAAGATGACAGTATGTTTA--- 537
QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200
DB 538 GTGGACAAT-----GAAGCTGCTGTGCTGACTTGCAAATGGCGCTTCCAAC 582
QY 201 MetPheSerPheArgValValHisProAsnGln-----ProAsnLeu--- 214
DB 583 CTATATCATTCGCGCTGACATCAGGCGACACACACACACATCTTCCTATCTTCAC 642
QY 215 LeuGluIleuGluIleuThrIleuSerHisAspLeuSerIleu 226
DB 643 CTTGAGATGATTTGAGAGCCATGAACCTTCGCTT 678

```

#### RESULT 8

US-10-104-580-2  
 ; Sequence 2, Application US/10104580  
 ; Publication No. US20030033628A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Straus et al.

? TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
 ? TITLE OF INVENTION: Poplar and other plant species.  
 ? FILE REFERENCE: 62486  
 ? CURRENT APPLICATION NUMBER: US/10/104,580  
 ? CURRENT FILING DATE: 2002-03-21  
 ? PRIOR APPLICATION NUMBER: 09/410,464  
 ? PRIOR FILING DATE: 1999-10-01  
 ? PRIOR APPLICATION NUMBER: 09/287,700  
 ? PRIOR FILING DATE: 1999-04-06  
 ? PRIOR APPLICATION NUMBER: 60/080,851  
 ? PRIOR FILING DATE: 1998-04-06  
 ? NUMBER OF SEQ ID NOS: 24  
 ? SOFTWARE: PatentIn Ver. 2.0  
 ? SEQ ID NO 2  
 ? LENGTH: 946  
 ? TYPE: DNA  
 ? ORGANISM: Populus balsamifera subsp. trichocarpa  
 ? FEATURE:  
 ? NAME/KEY: CDS  
 ? LOCATION: (1)..(684)  
 ? US-10-104-580-2

Alignment Scores:	
Pred. No.:	1,44e-61
Score:	611.00
Percent Similarity:	70.69%
Best Local Similarity:	55.17%
Query Match:	51.91%
DB:	14
	Gaps: 4
	Length: 946
	Matches: 128
	Conservative: 36
	Mismatches: 56
	Indels: 12
	Gaps: 4

US-10-690-246A-2 (1-227) x US-10-104-580-2 (1-946)

Qy	1	MeGlyArlgIyrlIegIunIelyslvslIegIuaenprOthAsnArgInValThr	20
Db	1	ATGGGTGTGGAAAGATTGAAATCAAGAAAGATCGAAACCACCAACGCAATCAC	60
Qy	21	TyTsErIyArIgrValGIyIleuIyIyIyValIyVgInIeuthrValIeuCysAsp	40
Db	61	TACTCGAAGGAAGAATGTATATTTTCAAGAAAGCCCAAGAACTACGTACTTTGGAT	120

QY 4 ALGGLNLSerLeuIleMetPheSerSerThrGlyValLeuAlaAspTyrCysSerPro 60  
 Db 121 GCTAGAGTCTCTTATCATGTTCTCTCCACACTAACCAACTCAATAGGATGACTTGGCCC 180  
 QY 61 SerThrAspIleYsgIyIleTyrGluIaGTrGlnValIvalThrGlyMetAspLeuTrp 80  
 Db 181 TTCACATCTGCACAAAGAGATCTGACATCAATATGCAAGCGCTTTGGGATGAGTCTGGG 240

Oy	8	Aaaalagintyrgtgmctgtaenthrileuylvghleuanenqliaasnglmasn	100
		.....:::..:::..:::	
Dd	241	GGCACTCMAACGAGAAAATCGAAGCACCTTGAGGAAGCTAAATGATTTCATTAAG	300
Oy	101	LeuarlgysglulleargatgatgtybglygtugluLeuengluglymetasprielleyscin	120
Dd	301	CTAGAGACAAGAATTCAGGCAGAGAGAGAGAGGGCTGTGAATGATCTTAGCATTTGATCAT	360
		.....:::..:::..:::	

[illegible]

Qy	16	TyRgRglaleuulIleHagIwleuAapmetyGluIuaaPaaAntTygIyPheasn	180
		.....	
Db	481	CATGAAACCTCTTGATGAAATTAAGCAAACTAGAGATCCACAGTATGGTTA---	53
		.....	
Qy	181	ValIuaaagInserArgIleTygIuaaenSerIlePrometValaAaGluCyapProGln	200
		.....	
Db	538	GTGACACAT-----GAAGCTGCTGTGGCACTTGCAAAATGGGGCTTCCAAc	582
		.....	

Qy 201 MetPheSerPheArgValValHisProAsnGln-----ProAsnLeu--- 214

Db 583 CTTATGCAATTCGGCCGTGATACGGGACAAACCAACCAACCATCTCCCTTAATCTTCAC 642

Qy 215 LeuG1LeuG1YtyrCluseR1aAp1useR1eu 226

Db 643 CTTGAGANTGATTTGAGCCCATATACCTTGCCCTT 678

RESULT 9  
US-10-487-901-7033

; Sequence 7033, Application US/10487901  
; Publication No. US20050091708A1

```

; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent

```

APPLICANT: McCreery, David  
; APPLICANT: Pell, Randy

APPLICANT: Miller, Barbara  
;  
APPLICANT: Weglarz, Thaddaus  
;

```

; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth

```

APPLICANT: Larrinua, Ignacio  
; APPLICANT: Reddy, Avutu

APPLICANT: Shukla, Vipula  
APPLICANT: Crosley, Rodney

; TITLE OF INVENTION: Nucleic Acid Co  
; FILE REFERENCE: DOW-08552

; CURRENT APPLICATION NUMBER: US/10/4  
 ; CURRENT FILING DATE: 2004-02-26

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; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 7033
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; LENGTH: 637

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; TYPE: DNA
; ORGANISM: Artificial
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; FEATURE:
; OTHER INFORMATION: Synthetic
;

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US-10-487-901-7033

Significant Occurs:	
Pred. No.:	1.07e-57
Score:	576.00
Percent Similarity:	84.87%
Best Local Similarity:	70.33%
Query Match:	48.94%
DB:	21
	Gaps:
	21

US-10-690-246A-2 (1-227) x US-10-487-901-7033 (1-637)

QY 1 MetcIARGGI'LVysIleGIuIIlelybysIleGIuaSnProThrAsnArgGIuValThr 20

D<sub>b</sub> 180 ATGGGAGGGCGCAAGATCGAATCAAGCGGAACTCGAACCGGCACAGCAGGTGACC 229  
Dy 21 TysSerItyARgArValGIlyleuleylsAlalysgIluLeuThrVallleuCyAsp 40  
Db 240 TACTCCAGAAGCGCGCACGGGAGTCAAGAAAGAGCGCAAGGCGCTCACCGGCTCTGGAC 299  
Dy 41 AAlaGlNValSerleulleulewetheserSerThrgilylSleualaaPyTySerPro 60

Db 300 GCCCAGGTGCGCATATCATGTTCTCTCCACCGGCAGATACACGAGTTCTGCAGCCCT 3529  
 Qy 61 SerThraPpILeYleGlyILeYrGluuArGrYrGlnValValILhrrGlyMeLaspLeuTrp 80  
 Db 360 TCCACCGACATCAAGGGGATCTTTTACCGCTACACGACGAGCCATCGGAGCAGGCTTTGG 419  
 Qy 81 AsnILaGILnYrGluuArGrwGcLInAsnThrLeuYrYhILeuaGnGILuILeAsrGlnAsn 1000

Dd 420 ATGCAGCAGTATGAGAAATTGGACGGCAAGCTGAGCCACTTCAGAGCATTAACCGGCAC 479

Oy 101 LeuAArgLysGIuIILeArqArqArgLyRgLYtLuLuLeuGlUGlYmeChapLIleYagIm 120

Dd 480 CTGGGCAACCGAGNTCTGGGAAAGATGTGAGAGAAGTTCTGGACGGGACTTGAGACTTCAGACG 539

Oy 121 LeuAArgGLYLeuclUGluInThrLeuclUGluSerLeuAArgIIleValARGHISargLYSTyr 140



Db 327 CTTCGTAAAGAGATTAGGACGAGATGGAGATTGCTGTGAACGATCTGGGATGGAAGAT 386  
 QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgGlyValArgHisArgGlyTyr 140  
 Db 387 CTCACACTCTTGAAGAGAAATGACAAAGCCGCAAGGTTGTTGCTGAGCGTAAGTAT 446  
 QY 141 HisValIleAlaThrGlnThrAspThrTyrLeuLeuLeuLeuLeuSerThrArgGluThr 160  
 Db 447 AAGGTATTAACAATACGATGTGACCCACAGAGAAAAGTTTAAATACAGAAAGAAAGT 506  
 QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLeuGluGluAsnProAsnTyrGlyPheAsn 180  
 Db 507 CACAAACAGACTCTGATGACTTGATGACAAAGCAGAAAGATCCAGCTTTGCATTG--- 563  
 QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGln 200  
 Db 564 ATGATAATGAGAGGGAG---TACGAGTCTGTGATCGAATTCGAATTTAAGTCCACGC 620  
 QY 201 MetPheSerPheArgValValHisProAsnGlnProAsn 213  
 Db 621 ATGTTGGATTGGAGC---CTACAGCCCAAGCCATCTTAGT 656

RESULT 12  
 US-10-425-114-10670  
 ; Sequence 10670, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E  
 ; APPLICANT: Tabaska, Jack E  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 10670  
 ; LENGTH: 871  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700958586\_FLI  
 US-10-425-114-10670

Alignment Scores:  
 Pred. No.: 5,1e-52 Length: 871  
 Score: 529.50 Matches: 103  
 Percent Similarity: 70.81% Conservative: 45  
 Best Local Similarity: 49.28% Mismatches: 58  
 Query Match: 44.99% Indels: 3  
 Gaps: 3

US-10-690-246a-2 (1-227) x US-10-425-114-10670 (1-871)

QY 5 LysIleGluIleuLysIleGluAsnProThrAsnArgGlnValThrTyrSerLysArg 24  
 Db 3 AAGATCCAGATCAAGAGATGAGAACACCAACCGCAGGTCACTTATTTCTAAACGA 62  
 QY 25 ArgValGlyIleLeuLysValAlaGluLeuThrValLeuCysAspAlaGlnValSer 44  
 Db 63 CGGAATGGCTTTTCAAGAAAGCCACAGAGCTCCGTTCTATAGCGATGCCAAGTTTCT 122  
 QY 45 LeuIleMetPheSerSerThrGlyLysLeuAlaAspTyrCysSerProSerThrAspIle 64  
 Db 123 ATATTATATGTTCTCCAGACACTGGGAAACTCCAGAGATACATACGCCCTCCACTCAACA 182  
 QY 65 LysGlyIleTyrGluArgGlyGlnValValThrGlyMetAspLeuThrAsnAlaGlnTyr 84  
 Db 183 AAGCAGTTCTTCGATCGATCAAGATGATGATCTGAGAGTCAATCTCTGAACTCTCATTAC 242

QY 85 GluArgMetGlnAsnThrLeuLysHisLeuAsnGluIleAsnGlnAsnLeuArgLysGlu 104  
 Db 243 GAGATATCCAGAGAACTGTAAGAACTCAAGAGTGTGAATGGAATCTTCGTAAAGG 302  
 QY 105 IleArgArgArgLysGlyGluGluGluGluGluMetAspIleLysGlnLeuArgGlyLeu 124  
 Db 303 ATTAGCGAGAGGATGGAGATGCTGTAACGATCTGGGCATCGAAGATCTCAAGCTCTT 362  
 QY 125 GluGlnThrLeuGluGluSerLeuArgIleValArgHisArgLysTyrHisValIleAla 144  
 Db 363 GAGAAAGAAATGACAAAGGCCCCCAAGGTGTGTGTAAGCTTAATGATTAAGTGTAA 422  
 QY 145 ThrGlnThrAspThrTyrLeuLysLysLeuLysSerThrArgGluThrTyrArgAlaLeu 164  
 Db 423 ATTCGATTGACACCCAAAGAAAGAAAGTTTAAATACGAAAGAAAGTGCACAAACGACTC 482  
 QY 165 IleHisGluLeuAspMetLeuGluGluAsnProAsnTyrGlyPheAsnValGluAsnGln 184  
 Db 483 CTGCGTGACTTGATGACAAAGACAGAGATCCACGTTTTCATTG---ATAGATATGGA 539  
 QY 185 SerArgIleTyrGluAsnSerIleProMetValAsnGluCysProGlnMetPheSerPhe 204  
 Db 540 GGGGAG---TACGAGTCTGTGATCGAATTCGAATTTAAGTCCACGATGTCGATTG 596  
 QY 205 ArgValValHisProAsnGlnProAsn 213  
 Db 597 AGC---CTACAGCCCAAGCCATCTTAGT 620

RESULT 13  
 US-10-021-323-8631  
 ; Sequence 8631, Application US/10021323  
 ; Publication No. US20040123340A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dekman, Jill  
 ; APPLICANT: Feng, Paul C.C.  
 ; APPLICANT: Fincher, Karen L.  
 ; APPLICANT: Ziegler, Todd E.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 38-21(52274)B  
 ; CURRENT APPLICATION NUMBER: US/10/021,323  
 ; CURRENT FILING DATE: 2001-12-12  
 ; PRIOR APPLICATION NUMBER: US 60/255, 619  
 ; PRIOR FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 17880  
 ; SEQ ID NO 8631  
 ; LENGTH: 644  
 ; TYPE: DNA  
 ; ORGANISM: Gossypium hirsutum  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1)..(644)  
 ; OTHER INFORMATION: unsure at all n locations  
 ; OTHER INFORMATION: Clone ID: LIB3828-013-Q1-K6-F12  
 US-10-021-323-8631

Alignment Scores:  
 Pred. No.: 4,3e-52 Length: 644  
 Score: 528.50 Matches: 108  
 Percent Similarity: 71.84% Conservative: 40  
 Best Local Similarity: 52.43% Mismatches: 56  
 Query Match: 44.90% Indels: 3  
 Gaps: 2

US-10-690-246a-2 (1-227) x US-10-021-323-8631 (1-644)

QY 1 MetGlyArgGlyLysIleGluIleuLysIleGluAsnProThrAsnArgGlnValThr 20  
 Db 32 ATGGCTCGAGGAGAAAGTCCAGATCAAGCTGATGAGAACTCCAGCAACGAGCAATCAG 91  
 QY 21 TyrSerLysArgArgValGlyIleLeuLysValAlaGluLeuThrValLeuCysAsp 40  
 Db 92 TATTGAAAGAAAGAAACGCTTTTCAAGAAAGCTAATGAAGCTTAAGTCTTTCGAT 151



QY 41 AlAGlnValSerleuIleMetPheSerSerThrGlyLeuAlaAspTyrCysSerPro 60  
DB 152 GCTAGAGTTTCATCATCATGTTTCCACTAGTGAATCCCACTGATTCAGCCCT 211  
QY 61 SerThrAspIleLeuGlyIleTyrGluArgTyrGlnValAlaThrGlyMetAlaPheTyr 80  
DB 212 TCCACCAACCAAGCAAGCAAGTATGATCACTACCAAGAAACCTTGGGATCGATCTGG 271  
QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuIleHisLeuAsnGlnIleAsnGlnAsn 100  
DB 272 AACACCCACTATGAGAAATGCAAGACAGCTGAAAGCACTGAAAGCTTAAACAGAAC 331  
QY 101 LeuArgGlySerGluIleArgArgGlyGlyGluGluGluGluGluGluGluGluGluGlu 120  
DB 332 CTCGGCAAGAGATGATGAGAAAGGATGGCGCACTGTTGAATGATTTGACATCGAAGAT 391  
QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluSerLeuArgIleValArgHisArgGlyTyr 140  
DB 392 CTGGTGCTTGGAAAGAAATGAGAGCTGTGTCACTTATTCGTGATGAAAGTAT 451  
QY 141 HisValIleAlaThrGlnThrAspThrTyrIleHisLeuLeuSerSerThrArgGluThr 160  
DB 452 CGGTTCCTCCCAACCAAGATCATCTTCCAGAAAAAGTGAAGAAATGCGAAGATA 511  
QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLeuGluGluGluGluGluGluGluGluGlu 180  
DB 512 CACAAAATCTCTTACATGAAATCCCTGAAGAAATGCA--TATGAAATTA-- 566  
QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValaAsnGluCysProGln 200  
DB 567 GTTATATATGAGGGGAT--TATGATATACCTGATCGGATCAAAATGAGAGTCTCGT 623  
QY 201 MetPheSerPheArgVal 206  
DB 624 ATATTGCTTTACGCTG 641

RESULT 14  
US-10-487-901-7174  
; Sequence 7174, Application US/10487901  
; Publication No. US20050091708A1  
; GENERAL INFORMATION:  
; APPLICANT: Oreido, Jeremiah Vincent  
; APPLICANT: McCreary, David  
; APPLICANT: Miller, Randy  
; APPLICANT: Pell, Barbara  
; APPLICANT: Weglarz, Thadeus  
; APPLICANT: Gachotte, Daniel  
; APPLICANT: Blakelee, Beth  
; APPLICANT: Larrina, Ignacio  
; APPLICANT: Reddy, Avutu  
; APPLICANT: Shukla, Yipula  
; APPLICANT: Crosley, Rodney  
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Character  
; FILE REFERENCE: DOM-08552  
; CURRENT APPLICATION NUMBER: US/10/487,901  
; CURRENT FILING DATE: 2004-02-26  
; NUMBER OF SEQ ID NOS: 7560  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7174  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-487-901-7174

Alignment Scores:  
Pred. No.: 2.78e-51 Length: 630  
Score: 521.50 Matches: 99  
Percent Similarity: 70.65% Conservative: 43  
Best Local Similarity: 49.25% Mismatches: 56  
Query Match: 44.31% Indels: 3

DB: 21 Gaps: 1  
US-10-690-246a-2 (1-227) x US-10-487-901-7174 (1-630)  
QY 1 MetGlyArgGlyLeuValIleGluIleLeuValIleGluAsnProThrAsnArgGlnValThr 20  
DB 34 ATGGCTCGTGGAGAAATGCCAGATCAAGAGAAATGAGAACCAACAAACAGACAAAGTCACT 93  
QY 21 TyrSerLeuArgArgValGlyIleLeuValIleGluValIleGluLeuThrValLeuCysAsp 40  
DB 94 TATTCTTAAGAGAAATGAGATGCTTCAAGAAAGCAATGAACTGCTGTTTGGAT 153  
QY 41 AlAGlnValSerleuIleMetPheSerSerThrGlyLeuAlaAspTyrCysSerPro 60  
DB 154 GCTAAAGTTCTATTAATATGATTTCAAGTACGAAAGAACTTATGATTAATTAAGTCT 213  
QY 61 SerThrAspIleLeuGlyIleTyrGluArgTyrGlnValAlaThrGlyMetAlaPheTyr 80  
DB 214 TCTGTACAGCAAGCAAGCTGTTGATCTGTATCAAAAGACTGTTGAGATTGATCTTGG 273  
QY 81 AsnAlaGlnTyrGluArgMetGlnAsnThrLeuIleHisLeuAsnGlnIleAsnGlnAsn 100  
DB 274 AACCTCCACTATGAGAAATGCAAGACAGCTTGAAGAAAGTAAAGATGTTAATGAGAT 333  
QY 101 LeuArgGlySerGluIleArgArgGlyGlyGluGluGluGluGluGluGluGluGluGlu 120  
DB 334 CTCGGAAGAGATGAGGCGAGAGATGGGAAAGCTTAAACGATCTGAATGAGCAG 393  
QY 121 LeuArgGlyLeuGluGlnThrLeuGluGluGluSerLeuArgIleValArgHisArgGlyTyr 140  
DB 394 TTGGAAGAGCTCAATGAAATGGAACAATCTCTGAAAGCTTATTCGTGAAGAAAGTAT 453  
QY 141 HisValIleAlaThrGlnThrAspThrTyrIleHisLeuLeuSerSerThrArgGluThr 160  
DB 454 AAAGTATGATGACATGATGAACTGAAACCTAACAGAAAGGTCGGAGATGCGAAGATA 513  
QY 161 TyrArgAlaLeuIleHisGluLeuAspMetLeuGluGluGluGluGluGluGluGluGlu 180  
DB 514 CATGAATCTCTTGAATTTGATGCAAGACAGAAAGCA--TATGCA 564  
QY 181 ValGluAsnGlnSerArgIleTyrGluAsnSerIleProMetValaAsnGluCysProGln 200  
DB 565 TTGTTAGCAAGAAAGGAGCTAATCACTGTGCTTGATTTCCAAATGAGGGCCACGC 624  
QY 201 Met 201  
DB 625 ATA 627

RESULT 15  
US-10-487-901-3483  
; Sequence 3483, Application US/10487901  
; Publication No. US20050091708A1  
; GENERAL INFORMATION:  
; APPLICANT: Oreido, Jeremiah Vincent  
; APPLICANT: McCreary, David  
; APPLICANT: Pell, Randy  
; APPLICANT: Miller, Barbara  
; APPLICANT: Weglarz, Thadeus  
; APPLICANT: Gachotte, Daniel  
; APPLICANT: Blakelee, Beth  
; APPLICANT: Larrina, Ignacio  
; APPLICANT: Reddy, Avutu  
; APPLICANT: Shukla, Yipula  
; APPLICANT: Crosley, Rodney  
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Character  
; FILE REFERENCE: DOM-08552  
; CURRENT APPLICATION NUMBER: US/10/487,901  
; CURRENT FILING DATE: 2004-02-26  
; NUMBER OF SEQ ID NOS: 7560  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3483  
; LENGTH: 664  
; TYPE: DNA

